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(54) Title: METHOD AND KIT FOR HLA CLASS I TYPING <p style="text-align: center;">GROUP-SPECIFIC NON-CODING REGION PRIMERS</p> (57) Abstract <p>The present invention relates to methods and materials for determining the HLA Class I type of a subject, wherein group-specific sequences are used to design primer molecules which may be used in amplification protocols which accurately identify the HLA group(s) and/or allele(s) carried by the subject.</p>		

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Description

Method And Kit For HLA Class I Typing

1. Introduction

The present invention relates to methods and materials for determining the HLA Class I type of a subject, wherein group-specific sequences are used to design primer molecules which may be used in amplification protocols which accurately identify the HLA group(s) and/or allele(s) carried by the subject.

2. Background Of The Invention

The Histocompatibility Locus Antigen ("HLA") Class I genes comprise three classical genes encoding the major transplantation antigens HLA-A, HLA-B, and HLA-C and seven other Class I genes of which HLA-E, HLA-F and HLA-G are probably functional genes and HLA-H, HLA-I, HLA-K and HLA-L are pseudogenes. The class I genes share a similar structure, which includes, *inter alia*, 5' → 3', a 5' untranslated flanking region; a first exon ("exon 1") having a length of approximately 73 base pairs ("bp"); a first intron ("intron 1") having a length of approximately 130 bp; a second exon ("exon 2"), having a length of approximately 250 bp; a second intron ("intron 2"), having a length of approximately 272 bp; a third exon ("exon 3"), having a length of approximately 276 bp; a third intron ("intron 3"), having a length of approximately 588 bp; and a fourth exon ("exon 4").

The HLA Class I genes are highly polymorphic among individuals. As of 1996, at least 73 alleles of HLA-A, 126 alleles of HLA-B and 35 alleles of HLA-C have been identified. This variability is of particular relevance when tissue transplantation between a donor and a host is contemplated. The histocompatibility antigens of donor and host should be as similar as possible to avoid both immune rejection of the transplanted tissue as well as graft-versus-host disease. It is therefore important to accurately identify the HLA types of donor and host. In view of the exigencies implicit in tissue transplantation, it is desirable that the typing be accomplished as efficiently as possible.

Methods for determining alleles of HLA-A, HLA-B, and HLA-C in a

patient sample have been heavily investigated because of the functional importance of these genes in transplant tissue matching and autoimmune diseases. The first tests developed used immunological methods to identify epitopes expressed by various HLA loci. These tests (e.g., the complement-dependent cytotoxicity assay described in Terasaki and McClelland, *Nature*, 204:998, (1964)) identified broad serological specificities but were not capable of distinguishing between allelic members of a group, and sometimes mis-identified groups altogether. Unfortunately, even the most accurate of such low resolution assays cannot detect and distinguish all functionally significant transplant antigens (Anasetti et al. *Hum. Immunol.*, 29:70 (1990)).

High resolution tests performed at the nucleic acid level which distinguish among alleles of each group have become the focus of recent research. Current methods of high resolution typing include the following.

The Sequence Specific Oligonucleotide Probes ("SSOP") technique, as described in United States Patent No. 5,451,512 assigned to Hoffman-La Roche, Inc., uses a reverse dot blot format, wherein HLA-A probes are immobilized on a membrane, and the labelled target (patient sample) DNA is hybridized to the membrane-bound probe (as described in Saiki et al., 1989, *Proc. Natl. Acad. Sci.* 86:6230-6234). The pattern of hybridization to the probes on the dot-blot gives information regarding the HLA type of the individual. However, because hybridization is inherently not sufficiently specific to rule out minor differences in sequence between probe and patient sample, there is a possibility that the patient sample may contain an allelic variant which is not accounted for.

Another nucleic acid-based test is the Amplification Refractory Mutation System (ARMS) as described in the "HLA Class I SSP ARMS-PCR Typing Kit" Reference Manual, June 1995 edition, published by the Imperial Cancer Research Fund. This assay is based on the need for complementarity (matching) between the 3' end of an amplification primer and a target DNA sequence. Absent such matching, the primer will not function properly and no fragment will be amplified. Sequence information is deduced by determining, for various pairs of primers acting on target DNA from a patient sample, whether or not a fragment is successfully amplified. The accuracy of the technique is limited by the number of

primer pairs tested and by the possibility that allelic variations exist in regions of DNA which lie between the primers.

In order to overcome the foregoing shortcomings, it has been proposed that typing be accomplished by direct DNA sequencing (Santamaria et al., "HLA Class I Sequence-Based Typing" Hum. Immunol. 37, 39-50 (1993); WO 9219771; US Pat. 5,424,184). However, while direct sequencing of a patient's Class I HLA locus may conceptually be the most accurate, such sequencing may require a time-frame unsuitable for clinical practice. The success of direct sequencing methods may be expected to rely upon the design of efficient protocols and relevant primer sequences.

Prior to the present invention, direct sequencing protocols have exhibited a number of disadvantages. For example, the method of Santamaria et al., *supra*, fails to provide sufficient information because it focuses on cDNA (exon) sequences which, in view of exon sequence diversity, offer a very limited selection of conserved primer hybridization sites. In addition, because the Santamaria sequencing primers hybridize within an exon, they do not provide information for DNA sequence upstream of the primer which is potentially decisive for distinguishing among alleles. Further, the sites disclosed were determined before the recent discovery of dozens of more alleles that now need to be considered in identifying HLA type.

Intron sequences could provide the preferred hybridization sites for amplification and sequencing primers for the HLA-A, HLA-B and HLA-C genes because they may provide the DNA sequence of the full exon. Intron sequences for an HLA Class I gene were disclosed at least as early as 1985 (Weiss et al Immunobiol 170:367-380, (1985)). Due to their substantial diversity, and the difficulties in sequencing, few intron sequences have been published subsequently.

A number of researchers have made limited use of intron based oligonucleotides for limited aspects of HLA Class I typing.

Blasczyk et al. (Tissue Antigens 1996: 47: 102-110) used exon based amplification primers to determine group specificity. After amplification, universal sequencing primers located in intron 2 were used to sequence the amplified fragment. The paper does not disclose any intron sequence motifs from intron 1 or 3 or the 5'

untranslated region.

Cereb et al. (Tissue Antigens 1995: 45:1-11), undertook the identification of intron sequences useful for locus-specific amplification primer sets for all Class I genes. These primer sets were designed to amplify all alleles of the same locus. No group specific amplification primers were sought or reported. Further, amplified fragments were characterized by SSOP and not by direct sequencing.

Johnston-Dow et al (Poster Presentation: 1995 ASHI Meeting, Dallas, TX) presented a system for direct sequence determination of HLA-A wherein degenerate exon based primers were used to amplify exons 1 to 5 of the genomic HLA-A DNA sequence. As in Cereb et al., supra, the degenerate primer pool was designed to amplify all alleles of the HLA-A locus. Group specificity was not sought or reported. Further, sequencing of the amplified fragment was obtained using a degenerate primer mix wherein primers hybridize to intron regions flanking exons 2 and 3.

A rational approach to typing of classical HLA Class I loci would provide a simplified series of steps for high resolution typing of each allele of each loci in a patient sample using intron based oligonucleotides. Further, this method would be able to identify new alleles without ambiguities.

3. Summary Of The Invention

The present invention relates to materials and methods for high-resolution, nucleic acid-based typing of the three classical HLA Class I genes (comprising the loci HLA-A, HLA-B and HLA-C) in a patient sample. It is based, in part, on the discovery of group-specific sequence motifs, derived from the analysis of numerous patient samples, which include sequences of the 5' flanking region, intron 1, intron 2, and intron 3. Such sequence motifs may be used to design amplification primers which may be used to identify the HLA group or type of a subject. The invention is also based, in part, on the determination of numerous allele-specific sequences which may be used to confirm the precise allelic type of a subject.

The present invention provides for substantially purified nucleic acids which are capable of selectively hybridizing with group specific sequence motifs in untranslated regions of the HLA-A, HLA-B or HLA-C gene loci. Such nucleic acids, which may be comprised in a kit, may be used, alone or in conjunction with exon-based primers, to determine the group specificity of HLA-A, HLA-B, or HLA-C alleles contained in a patient sample and to identify the specific alleles present.

In particular embodiments, the present invention provides for methods of ascertaining the HLA Class I type of a subject which comprise performing a first amplification reaction which identifies the group type of the subject, and a second amplification reaction which produces allele-specific nucleic acids for sequencing.

3.1. Definitions

"Allele" means one of the alternative forms of the gene in question;

"Amplification" means the process of increasing the relative abundance of one or more specific genes or gene fragments in a reaction mixture with respect to the other genes. A method of amplification which is well known by those skilled in the art is the polymerase chain reaction (PCR) as described in United States Patents Nos. 4,683,194, 4,683,195 and 4,683,202, which are incorporated herein by reference. The PCR process involves the use of pairs of primers, one for each complementary strand of the duplex DNA (wherein the coding strand is referred to as the "sense strand" and its complementary strand is referred to as the "antisense strand"), that will hybridize at a site located near a region of interest in a gene. Chain

extension polymerization (without a chain terminating nucleotide) is then carried out in repetitive cycles to increase the number of copies of the region of interest many times. The amplified oligonucleotides are then separated from the reaction mixture and used as the starting sample for the sequencing reaction. Gelfand et al. have described a thermostable enzyme, "Taq polymerase," derived from the organism *Thermus aquaticus*, which is useful in this amplification process (see United States Patent Nos. 5,352,600 and 5,079,352 which are incorporated herein by reference);

"Group" as used herein, refers to a subset of alleles of one loci, all of which share sequence features which distinguish them from other groups. For example, serological group reactivity (in a lymphocytotoxicity assay) is the conventional basis for nomenclature of HLA alleles. The first two digits of an allele refer to the serological group; for example, the designation A*0201, A*0202, A*0217 all are members of the A2 group. Further, typically the nomenclature refers to the serological split group (e.g., A23 and A24 are serological splits of A9;

"Group-specific sequence motif" means a generally short, 1-25 nucleotide ("nt") sequence of nucleic acid which is found only in one or a few groups. Where a motif is shared by several groups in one region of the HLA locus, group-specific sequence motifs in other regions of the locus may serve as group-distinguishing features. The motif may share one or more nucleotides with the consensus sequence for the region;

"Haplotype" means the allele present on one chromosome;

"Heterozygote" means the presence of at least two different alleles of a gene;

"Homozygote" means the presence of a single species of allele of a gene;

"Locus" means a gene, such as HLA-A, HLA-B or HLA-C;

"Locus specific" means an event or thing associated with only one locus;

"Patient sample" means a sample collected from a patient in need of HLA typing which contains a sufficient amount and quality of nucleic acid (preferably DNA) for the performance of an amplification reaction. A nonlimiting example of a suitable source is peripheral blood lymphocytes, tissue (including cell

cultures derived therefrom, mucosal scrapes, spleen and bone marrow;

"Primer" means a polynucleotide generally of 5-50 nucleotides length which can serve to initiate a chain extension reaction;

"Sequencing" or "DNA sequencing" means the determination of the order of nucleotides in at least a part of a gene. A well known method of sequencing is the "chain termination" method first described by Sanger et al., Proc. Nat'l Acad. Sci. (USA) 74(12): 5463-5467 (1977) (recently elaborated in EP-B1- 655506, and Sequenase 2.0 product literature (Amersham Life Sciences, Cleveland) incorporated herein by reference). Basically, in this process, DNA to be sequenced is isolated, rendered single stranded, and placed into four vessels. In each vessel are the necessary components to replicate the DNA strand, which include a template-dependant DNA polymerase, a short primer molecule complementary to a known region of the DNA to be sequenced, and individual nucleotide triphosphates in a buffer conducive to hybridization between the primer and the DNA to be sequenced and chain extension of the hybridized primer. In addition, each vessel contains a small quantity of one type of optionally detectably labeled dideoxynucleotide triphosphate, *e.g.*, dideoxyadenosine triphosphate ("ddA"), dideoxyguanosine triphosphate ("ddG"), dideoxycytosine triphosphate ("ddC"), or dideoxythymidine triphosphate ("ddT"). In each vessel, each piece of the isolated DNA is hybridized with a primer. The primers are then extended, one base at a time to form a new nucleic acid polymer complementary to the isolated pieces of DNA. When a dideoxynucleotide is incorporated into the extending polymer, this terminates the polymer strand and prevents it from being further extended. Accordingly, in each vessel, a set of extended polymers of specific lengths are formed which are indicative of the positions of the nucleotide corresponding to the dideoxynucleic acid in that vessel. These sets of polymers are then evaluated using gel electrophoresis to determine the sequence.

"Specific hybridization" means hybridization of one strand of a nucleic acid to its complement.

"Target sequence" means the preferred site for specific hybridization of a primer; and

"Untranslated region" refers to a portion of an HLA locus which is not transcribed into RNA and eventually translated into protein. Examples of untranslated regions are the 5' and 3' flanking regions and intron sequences. For example, the 5' flanking region is neither transcribed nor translated, and intron sequences are transcribed but not translated.

4. Description Of The Figures

FIGURE 1 is an illustration of the principle for an HLA class I sequencing strategy. Group-specific primers are used for PCR amplification, and universal primers located in the 2nd intron are used for sequencing, regardless of the amplified group. 5'FR= 5' flanking region; 5' UTR= 5' untranslated region (-1 to -23 from the ATG start codon in exon 1).

FIGURE 2A and 2B depict, in schematic form, a method of the invention in which a cocktail of HLA-A group specific primers is used to amplify target DNA contained in a patient sample. The products of amplification are then separated electrophoretically in an agarose gel, allowing the identification, by fragment mobility, of fragments corresponding to groups A2 and A3. Primers specific for groups A2 and A3 are then used to amplify duplicate samples of target DNA in separate reactions, to produce A2 and A3 fragments which may then be sequenced using universal sequencing primers. FIGURE 2C and 2D depict a strategy wherein group type specificity is determined by reaction of aliquots of genomic DNA in separate reactions with a panel of primer pairs.

FIGURE 3 depicts the nucleic acid sequences of the HLA-A 5' flanking region in various alleles, including a consensus sequence (SEQ ID NO:1) as well as the sequences for the following alleles: A*0101 (SEQ ID NO:2); A*0301 (SEQ ID NO:3); A*1101 (SEQ ID NO:4); A*1102 (SEQ ID NO:5); A*3001 (SEQ ID NO:6); A*3002 (SEQ ID NO:7); A*3004 (SEQ ID NO:8); A*0201-11 (SEQ ID NO:9); A*0215 (SEQ ID NO:10); A*0217 (SEQ ID NO:11); A*6801 (SEQ ID NO:12); A*6802 (SEQ ID NO:13); A*6901 (SEQ ID NO:14); A*2301 (SEQ ID NO:15); A*2402 (SEQ ID NO:16); A*2403 (SEQ ID NO:17); A*2404 (SEQ ID NO:18); A*2405 (SEQ ID NO:19); A*2407 (SEQ ID NO:20); A*2501 (SEQ ID NO:21); A*2601 (SEQ ID NO:22); A*3402 (SEQ ID NO:23); A*4301 (SEQ ID NO:24).

NO:24); A*6601 (SEQ ID NO:25); A*6602 (SEQ ID NO:26); A*6603 (SEQ ID NO:27); A*2901 (SEQ ID NO:28); A*2902 (SEQ ID NO:29); A*31012 (SEQ ID NO:30); A*3201 (SEQ ID NO:31); A*3301 (SEQ ID NO:32); A*3303 (SEQ ID NO:33); A*7401 (SEQ ID NO:34); A*7402 (SEQ ID NO:36); A*7403 (SEQ ID NO:37); and A*8001 (SEQ ID NO:38).

FIGURE 4 depicts the nucleic acid sequences of HLA-A intron 1 in various alleles, including a consensus sequence (SEQ ID NO:39) as well as the sequences for the following alleles: A*0101 (SEQ ID NO:40); A*0301 (SEQ ID NO:41); A*1101 (SEQ ID NO:42); A*1102 (SEQ ID NO:43); A*3001 (SEQ ID NO:44); A*3002 (SEQ ID NO:45); A*3004 (SEQ ID NO:46); A*0201 (SEQ ID NO:47); A*0202 (SEQ ID NO:44); A*0203 (SEQ ID NO:49); A*0204 (SEQ ID NO:50); A*0205 (SEQ ID NO:51); A*0206 (SEQ ID NO:52); A*0207 (SEQ ID NO:53); A*0207 (SEQ ID NO:54); A*0208 (SEQ ID NO:55); A*0209 (SEQ ID NO:56); A*0210 (SEQ ID NO:57); A*0211 (SEQ ID NO:58); A*0215 (SEQ ID NO:59); A*0217 (SEQ ID NO:60); A*6801 (SEQ ID NO:61); A*6802 (SEQ ID NO:62); A*6901 (SEQ ID NO:63); A*2301 (SEQ ID NO:64); A*2402 (SEQ ID NO:65); A*2403 (SEQ ID NO:66); A*2404 (SEQ ID NO:67); A*2405 (SEQ ID NO:68); A*2407 (SEQ ID NO:69); A*2501 (SEQ ID NO:70); A*2601 (SEQ ID NO:71); A*3402 (SEQ ID NO:72); A*6601 (SEQ ID NO:73); A*6602 (SEQ ID NO:74); A*6603 (SEQ ID NO:75); A*4301 (SEQ ID NO:76); A*2901 (SEQ ID NO:77); A*2902 (SEQ ID NO:78); A*3101 (SEQ ID NO:79); A*3201 (SEQ ID NO:80); A*3301 (SEQ ID NO:81); A*3303 (SEQ ID NO:82); A*7401 (SEQ ID NO:83); A*7402 (SEQ ID NO:84); A*7403 (SEQ ID NO:85); and A*8001 (SEQ ID NO:86).

FIGURE 5 depicts the nucleic acid sequences of HLA-A intron 2 in various alleles, including a consensus sequence (SEQ ID NO:87) as well as sequences for the following alleles: A*0101 (SEQ ID NO:88); A*0201 (SEQ ID NO:89); A*0202 (SEQ ID NO:90); A*0203 (SEQ ID NO:91); A*0204 (SEQ ID NO:92); A*0205 (SEQ ID NO:93); A*0206 (SEQ ID NO:94); A*0207 (SEQ ID NO:95); A*0208 (SEQ ID NO:96); A*0209 (SEQ ID NO:97); A*0210 (SEQ ID NO:98); A*0211 (SEQ ID NO:99); A*0215 (SEQ ID NO:100); A*0217 (SEQ ID NO:101);

A*6801 (SEQ ID NO:102); A*6802 (SEQ ID NO:103); A*6901 (SEQ ID NO:104); A*2501 (SEQ ID NO:105); A*2601 (SEQ ID NO:106); A*4301 (SEQ ID NO:107); A*6601 (SEQ ID NO:108); A*6602 (SEQ ID NO:109); A*6603 (SEQ ID NO:110); A*3402 (SEQ ID NO:111); A*2901 (SEQ ID NO:112); A*2902 (SEQ ID NO:113); A*3101 (SEQ ID NO:114); A*3201 (SEQ ID NO:115); A*3301 (SEQ ID NO:116); A*3303 (SEQ ID NO:117); A*7401 (SEQ ID NO:118); A*7402 (SEQ ID NO:119); A*7403 (SEQ ID NO:120); A*2301 (SEQ ID NO:121); A*2402 (SEQ ID NO:122); A*2403 (SEQ ID NO:123); A*2404 (SEQ ID NO:124); A*2405 (SEQ ID NO:125); A*2407 (SEQ ID NO:126); A*0301 (SEQ ID NO:127); A*1101 (SEQ ID NO:128); A*1102 (SEQ ID NO:129); A*3001 (SEQ ID NO:130); A*3002 (SEQ ID NO:131); A*3004 (SEQ ID NO:132); and A*8001 (SEQ ID NO:133).

FIGURE 6 depicts the nucleic acid sequences of HLA-A intron 3 in various alleles, including a consensus sequence (SEQ ID NO:134) as well as sequences for the following alleles: A*0101 (SEQ ID NO:135); A*0301 (SEQ ID NO:136); A*1101 (SEQ ID NO:137); A*1102 (SEQ ID NO:138); A*3001 (SEQ ID NO:139); A*3002 (SEQ ID NO:140); A*3004 (SEQ ID NO:141); A*0201 (SEQ ID NO:142); A*0202 (SEQ ID NO:143); A*0203 (SEQ ID NO:144); A*0204 (SEQ ID NO:145); A*0205 (SEQ ID NO:146); A*0206 (SEQ ID NO:147); A*0207 (SEQ ID NO:148); A*0208 (SEQ ID NO:149); A*0209 (SEQ ID NO:150); A*0210 (SEQ ID NO:151); A*0211 (SEQ ID NO:152); A*0215 (SEQ ID NO:153); A*0217 (SEQ ID NO:154); A*6801 (SEQ ID NO:155); A*6802 (SEQ ID NO:156); A*6901 (SEQ ID NO:157); A*2301 (SEQ ID NO:158); A*2402 (SEQ ID NO:159); A*2403 (SEQ ID NO:160); A*2404 (SEQ ID NO:161); A*2405 (SEQ ID NO:162); A*2407 (SEQ ID NO:163); A*2501 (SEQ ID NO:164); A*2601 (SEQ ID NO:165); A*3402 (SEQ ID NO:166); A*4301 (SEQ ID NO:167); A*6601 (SEQ ID NO:168); A*6602 (SEQ ID NO:169); A*6603 (SEQ ID NO:170); A*2901 (SEQ ID NO:171); A*2902 (SEQ ID NO:172); A*3101 (SEQ ID NO:173); A*3201 (SEQ ID NO:174); A*3301 (SEQ ID NO:175); A*3303 (SEQ ID NO:176); A*7401 (SEQ ID NO:177); A*7402 (SEQ ID NO:178); A*7403 (SEQ ID NO:179); and A*8001 (SEQ ID NO:180).

FIGURE 7 depicts a phylogenetic tree of the 5' flanking and 5' untranslated regions of HLA-A.

FIGURE 8 depicts a phylogenetic tree of introns 1-3 of the HLA-A gene.

FIGURE 9 depicts a phylogenetic tree of introns 1-3 of the HLA-B gene.

FIGURE 10 depicts the results of amplification using group-specific exon region primers to determine HLA-A group type, wherein the group specificity is determined to be 6601 and 3201 (see Table 7).

FIGURE 11 depicts the results of amplification using group-specific exon region primers to determine HLA-A group type, wherein the group specificity is determined to be 020x and 680x (see Table 8).

5. Detailed Description Of The Invention

The present invention relates to compositions and methods which may be used to efficiently and accurately determine the HLA Class I type of a patient sample.

The present invention is based, in part, on the determination of group-specific sequence motifs in regions of HLA Class I loci. These motifs may be used to design oligonucleotides which may be used as group-specific primers in nucleic acid amplification reactions. The present invention is also based, in part, on the determination of the sequences of regions of a wide variety of alleles of HLA Class I loci; such sequences may be used to distinguish one allele from another. Sequences of regions including the 5' flanking region of HLA-A and introns 1, 2 and 3 of HLA-A are provided herein, and are set forth in Figures 3-6.

In general, the methods of the invention may be described as follows. Comparison of nucleotide sequences of an HLA locus among members of an HLA Class I group, which lie in either untranslated or exon regions, may be used to identify group-specific motif sequences. Identification of groups may be by establishing serological relationships or using phylogenetic information, as set forth in Figures 7-9. Based on the group-specific motif sequences, oligonucleotide primers may be designed, synthesized, and used to amplify a portion of the HLA locus. Oligonucleotides used in this manner are referred to herein as "group-specific

primers" and, in particular, as "group-specific untranslated region primers" or "group-specific exon region primers", as the case may be.

In preferred nonlimiting embodiments of the invention, the primers correspond to untranslated regions of the HLA Class I locus ("group-specific untranslated region primers"). Such primers may be used in pairs, wherein each member of the pair hybridizes to an untranslated region lying on either side of at least one exon. For example, but not by way of limitation, primer pairs may be oligonucleotide pairs which hybridize to group-specific motifs in the 5' untranslated region and the first, second, or third intron; the first intron and the second or third intron; or the second and third intron.

The group-specific primers may be used in several different methods according to the invention. In a first series of nonlimiting embodiments, the group-specific primers may be used in a diagnostic manner to identify which allelic groups are present in a patient sample. In a second series of nonlimiting embodiments, the group-specific primers may be used to amplify sufficient amounts of a particular allelic fragment which is then subjected to direct nucleotide sequencing using universal sequencing primers.

According to the first series of embodiments, the present invention provides for a method of determining the HLA Class I group type of a subject comprising (i) combining a group-specific primer pair with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur; and (ii) determining whether a nucleic acid product is produced by the amplification; wherein the ability of a primer pair to produce a nucleic acid product is associated with a particular HLA group type. The group-specific primers may be group-specific exon region primers or group-specific untranslated region primers. In related embodiments the present invention provides for a method of determining the HLA Class I group type of a subject comprising (i) combining a plurality of group-specific exon region primer pairs with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur; (ii) determining the size of the nucleic acid products of the amplification; and (iii) correlating the size of the product with the predicted size of a fragment associated

with a particular HLA group type. The plurality of primers is referred to as an HLA "cocktail" (see Figures 1 and 2). These first methods may be used to provide useful diagnostic information. For example, group type determination may serve as a first level of comparison for a histocompatibility analysis, even without identification of the specific allele(s) involved. For example, if a potential donor and host are being evaluated for tissue transplantation, if it is found that their group types do not match, no further comparison may be necessary. If, alternatively, their types do match, further analysis, for example by direct sequencing, may be desirable.

According to the second series of embodiments, the present invention provides for a method of determining the HLA Class I allelic type of a subject comprising (i) combining a group-specific oligonucleotide primer pair with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur; (ii) collecting the nucleic acid product of the amplification; and (iii) determining the nucleic acid sequence of the product. The group-specific primer pair used may be determined based on the group type of the subject, as determined using the first method, described above. In preferred embodiments of the invention, group-specific untranslated region primers which span a region of the HLA locus containing allele-specific sequence may be utilized. If a subject is heterozygous, separate amplification reactions are performed for each group identified (e.g., separate reactions to amplify fragment for group A2 and group A3; see Figure 2). Sequencing may be performed using universal sequencing primers which will operate irrespective of HLA group or allelic type.

A more detailed description of the invention follows. Most alleles of the classical HLA Class I gene loci (consisting of HLA-A, HLA-B and HLA-C) can be distinguished on the basis of exon 2 and 3 alone. In one non-limiting embodiment, a method of the invention takes advantage of this fact, and employs the strategy generally described in Figure 2, using the example of HLA-A. A genomic DNA sample is prepared from a patient sample according to well known techniques. Aliquots of the genomic DNA may then separately be reacted with a panel of group-specific exon region primer pairs (Figure 2C), wherein the successful amplification of a DNA fragment is associated with a particular group type. Alternatively, as depicted

in Figure 2A), part of the sample may be treated with a cocktail of group-specific exon region primer pairs. Each primer pair in the cocktail will amplify only selected allelic groups because they specifically hybridize to group specific intron sequence motifs. Between them, under suitable polymerase chain reaction (PCR) conditions, the cocktail may amplify all known HLA-A groups, with each group specific amplification product having a different length. When reaction products are separated on an agarose gel the group(s) present in the patient sample may be identified by length.

Optionally, once the group specificity is determined, the direct sequence of alleles may be determined for precise allelic identification. As illustrated in Figure 2 B), a further part of the patient sample DNA may be treated under PCR conditions with a pair of primers that are specific for the previously determined group; preferably such primers are group-specific untranslated region primers, which span greater distances of the locus. If two groups were detected, then two separate reactions are performed. At completion of the second amplification, the reaction products are sequenced using an intron based "universal primer" which hybridizes to an intron sequence which is conserved among all alleles of the locus. Though it is theoretically possible to use a sequencing primer which is specific for the amplified group only, it is found that using a universal primer simplifies the method and the preparation of a kit. Various universal sequencing primers are specifically provided herein (see *infra*) which hybridize, respectively, to intron sequences flanking the 5' end of exon 2, the 3' end of exon 2, the 5' end of exon 3 and the 3' end of exon 3.

The substantial advantage of the method of the invention is that the initial group specific amplification allows a PCR based separation of haplotypes in 95% of patient samples. The separation of the haplotypes is a major achievement of this protocol since it permits the resolution of cis/trans linkages of heterozygote sequencing results which cannot be achieved with other protocols. With the instant invention, a separation of the haplotypes may be achieved in serological heterozygous samples with the sequencing primer mixes ("PMs") described in Table 2 (*infra*) using group-specific amplification corresponding to the serological families. The selection of the PMs used for sequencing depends on the amplification patterns of the preceding

PCR-SSP low-resolution typing. The primers are designed to work with a in a single cycle protocol including, but not limited to, a PCR protocol on a Perkin Elmer System 9600, maintaining typing capacities of the laboratory. All PCR products carry sufficient sequence information for a complete subtyping. This approach is superior to a typing system using a single pair of generic primers followed by direct sequencing or SSO hybridization, even if the amplification strategy is locus-specific. The substantial advantage of Sequence Based Typing (SBT) is the definition of the cis/trans linkage of sequence motifs. SBT after generic PCR amplification cannot define the cis/trans linkage of sequence motifs and therefore mimics oligotyping. The rapidly growing number of newly identified alleles confirms that new alleles have arisen mainly from gene conversion events which have usually taken place between different alleles of the same locus. Newly identified alleles are not characterized by new sequence motifs, but by a new combination of already existing sequence motifs. From this observation it may be concluded that the amount of alleles at each locus may theoretically represent all possible combinations of known sequence motifs. Of course, some of them will fall victim to negative selection. Nevertheless, it can be expected that still an enormous amount of alleles are yet unidentified. PCR-SSP subtyping strategies using a restricted number of oligonucleotides which do not cover all possible sequence motifs suffer from this limitation. If the cis/trans linkage of the analyzed polymorphic regions is not defined some new alleles may be mistyped as a heterozygous combination of known alleles. This has consequences with respect to SBT strategies. An unambiguous typing result of SBT after generic PCR amplification is only unambiguous with regard to the presently known HLA sequence databank. However, with the detection of new alleles this result can become ambiguous over the course of time. This observation has already been made in PCR based DRB1 typing during the last five years and will probably also occur in PCR based class I typing. Considering the above points, the idea of the instant SBT approach is not only to identify the HLA-A, HLA-B and HLA-C subtypes, but to cover as many of the polymorphic sites as possible and to define the cis/trans linkage of the polymorphic sequence motifs. Typing results obtained with this method will remain unambiguous independently of the growing HLA sequence databank.

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In general, group-specific primers are desirably designed to facilitate hybridization to their intended targets. It should be taken into account that homology between different groups, and indeed between group-specific motifs, may exist. Accordingly, in preferred embodiments of the invention, a primer may be designed such that it hybridizes to its group target under relatively stringent conditions. For example, one or more mismatched residues may be engineered into the 3' domain of the molecule. Further, the primer may be designed such that it differs from any naturally occurring or consensus sequence, but rather has mismatches inserted which serve to further reduce hybridization of the primer to target DNA of a group other than the intended target group. Under certain circumstances, one or more mismatches may be introduced into the 5' end to destabilize internal hairpin loops; such changes are not generally expected to enhance the efficiency of the primer.

The following nucleic acid sequences may be comprised in group-specific untranslated region primers for HLA-A which are specific for the groups as indicated in Table 1.

Table 1.

Designation	Sequence	N	Tm	Specificity	Position
II-210m	S 5' ACC Cgg gAA gCC ggg CCT 3'	18	64 C	A10 et al.	73-92
II-230m	S 5' ggC Agg TCT CAG CgA Ctg 3'	18	60 C	A*01,03,11,30	102-119
II-226	S 5' CTC TgT ggg gAg AAG CAA C 3'	19	60 C	A*02	29-47
II-221m11	S 5' ggg AgC ggC gCC ggg AC 3'	17	64 C	A*0301	77-93
II-209	S 5' gAA gCA Agg ggC Ccg CCC	18	64 C	A10 et al.	41-58
II-214m	S 5' CgC CTg gCg ggg gGg CAA 3'	18	66 C	A*2301,24	54-71
II-223d	S 5' gTg AgT gCg ggg TCg Tgg 3'	18	62 C	A19	1-19
II-225m	S 5' gCC ggg Agg Agg gAC ggT 3'	18	64 C	A*30	86-103
II-237m14	S 5' ggC gCg CCC ggC ggg gA 3'	17	65 C	A*29	49-65
II-240	S 5' ggA ggA ggg Tcg ggC ggA 3'	18	64 C	A*31,33	90-107
5'FL-243	S 5' AgT gTC TTC gCg gTC gCT C 3'	19	62 C	A*11	53-71
5'FR-257	S 5' CTC AgA TTC TCC CCA gAC g 3'	19	60 C	A all, except for A*11 6-24	
5'FR-273	S 5' CAT gCC gAg ggT TTC TCC CA 3'	20	64 C	A*28,6602,6603	360-380
BP202	S 5' CTg gCC CTg ACC CAg ACC A 3'	19	64 C	A*7401,7403	Exon 1, 49-68
BP203	S 5' CCT gAC CCA gAC CTg ggC A 3'	19	64 C	A*8001	Exon 1, 55-73
BP142	AS 5' C AGG TAT CTG CGG AGC CCG 3'	19	64 C	A*0101/**24	227-245
I3-236	AS 5' gTC TgT CAg gAA gAg TCA gAA 3'	21	62 C	A*non 02.28	584..+2
I3-239	AS 5' gTg gAA AAT TCT AgT CCC TgA A3'	22	62 C	A*multi,notA1,3,11,30.9	415-436
I3-246	AS 5' AgA TCT ACA ggC gAT CAg gA 3'	20	60 C	A*30	24-43
I3-247m6	AS 5' gCC AgC CCg gAg gTT CTA T 3'	19	62 C	A*01,11	36-54
I3-249	AS 5' CAg AgT CAC TCT CTg gTA Cag	21	62 C	All A,weak	59,70,92, J,E,G,F 148-168
I3-280m18	AS 5' gCg ATC gTC TTC CCg TCA C 3'	19	62 C	A*01,03,11,30	221-239
I3-282	AS 5' AgA gTC ACT CTC Tgg TAC AgA 3'	21	62 C	A*8001	148-168

The sequences in Table 1 have the following sequence identifiers: Il-210 is SEQ ID NO:35 and the remaining sequences Il-230m through Il-282 have SEQ ID NO:181-202, respectively.

The present invention provides for nucleic acid molecules comprising regions having the foregoing sequences or their functional equivalents.

"Functional equivalents" of a nucleotide sequence, as defined herein, refers to nucleotide sequences which, when contained in a nucleic acid molecule, retain the specificity of the disclosed sequence and/or hybridize to the complement of the disclosed sequence under stringent hybridization conditions (*e.g.*, $1 \times \text{SSC}$ at 65°C).

In specific nonlimiting examples, oligonucleotides comprising the above sequences, or functional equivalents thereof which retain specificity, may be used in a PCR amplification reaction in the following pairwise combinations to generate group specific fragments of the lengths as indicated in Table 2.

Table 2.

No.	Primer Mix	Sense Primer	Antisense Primer	Size of Product	HLA-A Specificity
1	1.1	I1-230m	BP142	785 bp	A*01
2	1.2	5'FR-257	I3-247m6	1068 bp	A*01
3	1.3	I1-230m	I3-247mg	870 bp	A*01,11
4	2	I1-226	I3-249	1056 bp	A*02
5	3	I1-221m11	I3-280m18	1078 bp	A*03
6	11	5'FL-243	I3-249	1229 bp	A*11
7	9	I1-214m	I3-249	1033 bp	A*23,24
8	10.1	I1-210m	I3-236	1450 bp	A*10
9	10.2	I1-210m	I3-249	1014 bp	A*10,68,69
10	28	5'FR-273	I3-249	1537 bp	A*68,69, 6602,6603
11	19.1	I1-223d	I3-239 or I3-249	1084 bp	A*29,31,32, 33,74
12	19.2	I1-240	I3-249	996 bp	A*31,33
13	29	I1-237m14	I3-249	1037 bp	A*29
14	30	I1-225m	I3-249	1000 bp	A*30
15	74	BP202 (Exon 1)	I3-249	1109 bp	A*7401, 7403
16	80	BP203	I3-282	1103 bp	A*8001 (untested)

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The following nucleic acid sequences may be comprised in group-specific exon region primers for HLA-A which are specific for the groups as indicated in Table 3 (sense primers) and Table 4 (antisense primers). The present invention provides for nucleic acid molecules comprising regions having the foregoing sequences or their functional equivalents. They may, in specific nonlimiting examples, be used in pairs as set forth in Table 5. The sequences in Table 3, primer numbers 85, 118, 120, 123, 127, 129, 134, 137, 140, 160, 167, 175, 193 and 202 have SEQ ID NO:203-216, respectively. The sequences in Table 4, primer numbers 98, 115, 116, 117, 126, 133, 135, 136, 138, 142, 144, 145, 152, 153, 154, 155, 161, 165, 168 and 180, have SEQ ID NO:217-236, respectively, and primer number 119 has SEQ ID NO:245.

Table 3.

Primer Number	Localization	Sequence
85	Exon 2 -4 - 5	5' CTC CTC gTC CCC Agg CTC T 3'
118	Exon 2 6 - 19	5' TCC ATg Agg TAT TTC TAC ACC 3'
120	Exon 3 -6 - 12	5' ggC CAg gTT CTC AgA CCA 3'
123	Exon 2 36 - 53	5' CCC ggC CCg gCA gTg gA 3'
127	Exon 3 1 - 20	5' gTT CTC ACA CCA TCC AgA Tg 3'
129	Exon 3 4 - 25	5' TCA CAC CCT CCA gAT gAT gTT 3'
134	Exon 3 63 - 80	5' ggg TAC CAg CAg gAC gCT 3'
137	Exon 2 9 - 29	5' TCC ATg Agg TAT TTC ACC ACA 3'
140	Exon 3 -1 - 20	5' ggT TCT CAC ACC ATC CAg ATA 3'
160	Exon 3 1 - 20	5' gTT CTC ACA CCA TCC AgA gg 3'
167	Exon 2 54 - 71	5' gAg CCC CgC TTC AAC gCC 3'
175	Exon 3 63 - 71	5' CTT CCT CCg Cgg gTA TgA A 3'
193	Exon 2 167 - 184	5' gCC ggA gTA TTg ggA CCg 3'
202	Exon 1 49 - 67	5' CTg gCC CTg ACC CTg ACC A 3'

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Table 4.

Antisense primers

Primer Number	Localization	Sequence
98	Exon 2 226 - 243	5' gCA ggg TCC CCA ggT CCA 3'
115	Exon 3 195 - 213	5' CCT CCA ggT Agg CTC TCA A 3'
116	Exon 3 195 - 213	5' CCT CCA ggT Agg CTC TCC A 3'
117	Exon 3 195-213	5' CCT CCA ggT Agg CTC TCT g 3'
119	Exon 2 184 - 203	5' CTT CAC ATT CCg TgT CTC CT 3'
126	Exon 3 212 - 230	5' CCA CTC CAC gCA CgT gCC A 3'
133	Exon 2 229 - 246	5' ggA gCg CgA TCC gcA ggC 3'
135	Exon 3 216 - 234	5' ggA gCC ACT CCA Cgg ACC g 3'
136	Exon 3 216 - 233	5' gAg CCA CTC CAC gCA CTC 3'
138	Exon 2 186 - 206	5' ggC CTT CAC ATT CCg TgT gTT 3'
142	Exon 3 228 - 246	5' CAg gTA TCT gCg gAg CCC g 3'
144	Exon 2 165 - 184	5' Tgg TCC CAA TAC TCA ggC CT 3'
145	Exon 2 226 - 243	5' gCA ggg TCC CCA ggT TCg 3'
152	Exon 3 163 - 179	5' ggg CCg CCT CCC AgT TgT 3'
153	Exon 2 179 - 197	5' TCT gTg AgT ggg CCT aCA CA 3'
154	Exon 2 184 - 204	5' CCT TCA CAT TCC gTg TCT gCA 3'
155	Exon 3 216 - 233	5' gAg CCA CTC CAC gCA CgT 3'
161	Exon 2 209 - 228	5' CCA CTC ggT CAg TCT CTg AC 3'
165	Exon 3 105 - 124	5' gAg CgCA ggT CCT CgT TCA A 3'
168	Exon 2 198 - 217	5' gTC TgT gAg Tgg gCC aTC AT 3'
180	Exon 2 12 - 31	5' CAg CCA TAC ATC CTC Agg AC 3'

Table 5.

Primer Mix No. Name		Sense Primer	Antisense Primer	Size of Product	HLA-A Specificity
1	1	140	142	247 bp	A*0101,0102,8001
2	2	85	98	256 bp	A*0201-0220
3	3	140	126	230 bp	A*0301,0302,0303
4	36	167	168	164 bp	A*0101,3601
5	11	118	119	195 bp	A*1101-1103
6	23	129	115	209 bp	A*2301
7	24	129	116+117	209 BP	A*2402-2411
8	10.1	160	135	233 bp	A*2501,2601- 2603,2605,4301,6601
9	25	118	133	238 bp	A*2501,2502
10	26	118	145	235 bp	A*2601,2602,2604,4301
11	34	134	155	171 bp	A*3401,3402
12	6602	134	136	240 bp	A*6602,6603
13	10.2	118	161	222 bp	A*11,34,6601,6602,68011, 6802,6901
14	43	118	154	196 bp	A*4301
15	68	120	152	185 bp	A*68011,68012,6802,6803
16	69	193	180	375 bp	A*6901
17	19	127	165	124 bp	A*2901,2902,31012,3201, 3301-3303, A*7401-7403
18	29	137	145	236 bp	A*2901,2902
19	30	175	115+116	162 bp	A*3001-3002
20	31	167	144	176 bp	A*31012
21	32	167	133	159 bp	A*3201,3202,2501,2502
22	33	137	138	198 bp	A*3301-3303
23	74	202	153	370 bp	A*7401,7403
24	80	140	136	234 bp	A*8001

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In general, the foregoing group-specific primers may be modified by addition, deletion, or substitution of bases, to produce functionally equivalent primers with the substantially the same specificity, that is to say, such that the group specific polymorphism(s) are not removed. Such modifications may be constrained by several parameters. First, exact matching at the 3' end is particularly important for primer extension. Preferably, at least 5 nt are complementary to target DNA. When the exactly conserved region is short, for example, less than 10 nt, it is not advisable to change the primer sequences. The primer is preferably less than 50% G or C. Also, the primers should be designed to avoid specific hybridization with pseudogenes or non-classical HLA Class I loci. In the examples which follow, the melting temperature of all primers used was about 62C to ensure uniform amplification conditions.

For sequencing purposes, the following nucleic acid sequences are sequences which hybridize to all alleles of the indicated loci, in the locations indicated (and hence are referred to as universal sequencing primers).

Table 6:

Universal Sequencing Primers for HLA-A

Desig.	Sequence	Location	Melting Temp.
5'-Ex2(Aw3)	5' GCG CCG GGA GGA GGG TC 3'	Int-1	Tm=58-62°C
3'-Ex2	5' ATC TCG GAC CCG GAG ACT 3'	Int-2	Tm=58°C
5'-Ex3	5' GTT TCA TTT TCA GTT TAG GCC A 3'	Int-2	Tm=60°C
3'-Ex3(Aw6)	5' CGG GAG ATC TAC AGG CGA TCA GG 3'	Int-3	Tm=58-62°C

Desig.	Sequence	Location	Melting Temp.
5'-Ex2(Aw3)	5'GCG CCG GGA GGA GGG TC 3'	Int-1	Tm=58-62°C
3'-Ex2	5'GTC GTG ACC TGC GCC CC 3'	Int-2	Tm=58-62°C
5'-Ex3	5'GGG CGG GGC GGG GCT CGG G 3'	Int-2	Tm=58-62°C
3'-Ex3(Aw6)	5'CGG GAG ATC TAC AGG CGA TCA GG 3'	Int-3	Tm=58-62°C

Desig.	Sequence	Location	Melting Temp.
5'-Ex2(Aw3)	5' GCG CCG GGA GGA GGG TC 3'	Int-1	Tm=58-62°C
3'-Ex2(ABCw1)	5' GGT CGT GAC CT(T/C)CGC CCC 3'	Int-2	Tm=58-62°C
5'-Ex3(ABCw2)	5' CCC GGT TTC ATT TTC 3'	Int-2	Tm=58-62°C
3'-Ex3(Aw6)	5'CGG GAG ATC TAC AGG CGA TCA GG 3'	Int-3	Tm=58-62°C

The primers in Table 6 are assigned, consecutively, SEQ ID NO: 237-

244.

The foregoing three groups of primers include 5' and 3' primers for sequencing across exons 2 and 3, respectively.

The selection of suitable universal sequencing primers is constrained by a variety of rules including the following. Sequencing primer hybridization sites must lie within the fragment amplified by the group specific amplification primers. All primers are desirably selected to provide informative sequence and not start too far downstream of useful sequence. Preferred primers hybridize to conserved sites near the exon/intron boundaries.

Direct sequencing of the 2nd and 3rd exon may be performed from either the 5' or 3' end using the primers of Table 6 *supra* which are located in conserved regions of the 1st, 2nd and 3rd intron as indicated. These conserved regions were found to be identical in all samples investigated, regardless of the amplified group.

An important issue of direct sequencing for HLA class I genes is the generation of a specific PCR product, which is rather complicated due to the

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extensive sequence homologies between the different HLA class I loci including several pseudogenes. If an adequate PCR product has been generated, any sequencing chemistry should be applicable.

In the normal case, since group specific amplifications take place before sequencing, only one allele at a time is sequenced, resulting in unambiguous homozygous sequencing results. In these cases alleles are relatively easy to identify, even without software.

However, in about 5% of cases, both alleles come from the same group, but the sequence results show heterozygosity. In practice, when viewed by a fluorescence-detecting system, the sample appears as a normal sequence of bases with, sporadically, two bases at one site, each with half the peak height. This result flows from the high degree of similarity shared among all alleles of each HLA gene; sequence heterozygosity flows from base substitutions. The laborious task of determining which alleles are present in the test sequence may be simplified using computer analysis. A software program called GeneLibrarian developed by Visible Genetics, the assignee of the present application, rapidly compares the test sequence to a database which includes all possible homozygote and heterozygote combinations of the alleles. The program identifies those stored sequences that are closest matched to the test sequence. The operator can then determine which allelic pair is in the test sample. If no allelic pair shows an exact match, the software allows the operator to review the test sequence to determine if errors in base-calling or other artifacts are interfering with the analysis.

The order of sequencing reactions may be selected by the operator. Each exon of each locus may be sequenced on the sense strand or anti-sense strand. A preferred method is to obtain sequence from one strand from each exon. If the results contain ambiguities, then the amplicon is re-sequenced using the other primer for the same exon. The availability of both sequencing primers provides redundancy to ensure robust results.

In some cases, it may be advantageous to employ an equimolar mixture of 2 or more oligonucleotide species. Mixtures of oligonucleotides may be selected such that between them they will effectively prime the sequencing reactions for all

alleles of the locus at the same site.

In an alternative technique, instead of using dye terminators, a dye-labelled primer may be employed. In this case, the selected sequencing primers is labelled on the 5' end with a detectable label, using phosphoramidite or NHS/dye ester techniques well known in the art. The label selected depends on the detection instrument employed. The label for use with an OpenGene System (Visible Genetics Inc., Toronto, ON) is the fluorophore Cy5.5 (Amersham Life Sciences, Cleveland OH). Fluorescein-isothio-cyanate may be used for detection with the ALF Automated Sequencer (Pharmacia, Piscataway NJ). In this method, which is well known to one skilled in the art, the sequencing reaction mixture is changed slightly to include only one ddNTP per reaction mixture. For detection of reaction products, the sample may be mixed with an equal volume of loading buffer (5% ficoll plus a coloured dye). 1.5 ul of these samples may be loaded per lane of a MicroCel electrophoresis cassette loaded in a MicroGene Blaster automated DNA sequencer (Visible Genetics Inc., Toronto). The sample may be electrophoresed and read.

Results may be displayed and analyzed with GeneObjects software. The sequence of bases may be determined, and the HLA allele to which the sequence corresponds may then be identified. This process may be performed for each locus (HLA-A, HLA-B, HLA-C) and the results may then be reported to the patient file.

It is well known in the art that different variations of sequencing chemistry may be employed with different automated DNA sequencing instruments. Single dye instruments, such as the OpenGene System (Visible Genetics Inc., Toronto), the ALF Express (Pharmacia, Uppsala, Sweden) or the Li-Cor 4000L (Lincoln City, Nebraska) generally use dye-labeled primers. In these systems a single chain termination sequencing reaction mixture is run per lane.

Multi-dye sequencers, such as the Prism 377 (Applied Biosystems, Inc., Foster City, California) detect multiple dyes in a single lane. This technology conveniently employs dye-terminator chemistry, where the chain-terminating nucleotides are themselves labeled with fluorophores (see United States Patent No. 5,332,666, to Dupont de Nemours and Co.). In this case, the reaction products carrying four different labels may be run in a single lane.

Either single dye or multi-dye chemistry may be employed according to the present invention, along with other sequencing chemistries. Additional methods for reducing the numbers of reactions required to obtain detailed sequence information from the classical HLA Class I loci are disclosed in commonly owned United States Patent Applications USSN 08/577,858 (for single-track sequencing) and USSN 08/640,672 and 08/684,498 (for single-tube sequencing), incorporated by reference herein.

The nucleic acids described above may be comprised in a kit for use in practicing the methods of the invention. In addition to the group-specific primers and primer pairs disclosed, such kits may further comprise buffers, reagents, and enzymes such as, amplification enzymes including but not limited to, *Taq* polymerase. In specific, non-limiting embodiments, the kit may comprise group-specific exon region primers (for example, as a "cocktail" comprising a plurality of primers) as well as group-specific untranslated region primers; such primers may be contained in individual tubes.

6. Example: Determination Of HLA-A Group Type

Genomic DNA was prepared from patient samples according to standard methods, such as a standard salting-out procedure (as provided by the Puregene DNA Isolation Kit, Gentra Systems, Inc., Minneapolis) or by detergent and proteinase K treatment (Current Protocols in Molecular Biology, Eds. Ausubel, F.M. et al, (John Wiley & Sons; 1995)).

All primers were synthesized on a Gene Assembler plus (Pharmacia, Uppsala, Sweden), and purified by fast protein liquid chromatography. The sequence, length, melting temperature (T_m), group specificity localization of the primers are given in Tables 3 (sense primers), 4 (antisense primers) and 5 (primer pairs). Internal positive control primers were: 5' primer hGHI 5'GCC TTC CCA ACC ATT CCC TTA 3', 21mer, $T_m=64^\circ\text{C}$, nucleotide position 5560-5580; 3' primer hGHI 5' TCC ATG TCC TTC CTG AAG CA 3', 20mer, $T_m=60^\circ\text{C}$, nucleotide position 6614-6633. These control primers amplify a 1074 bp fragment of the human growth hormone gene.

Group-specific identification was performed as follows. Aliquots of

genomic DNA were separately reacted with a panel of 24 group-specific exon region primer pairs set forth in Table 5, *supra* (see Blasczyk et al., 1995, Tissue Ant. 46:86-95). An amplification cocktail for pairs of primers was prepared in 10 μ l volume using standard 10x Perkin-Elmer buffer (1x buffer: 50 mM KCl; 1.5 mM MgCl₂; 10 mM Tris-HCl, pH 8.3; 0.001% (w/v) gelatin) supplemented with 5% glycerol and 0.1 μ l Cresol-red, sodium salt (Cresol-red stock solution: 10 mg/ml). The use of glycerol and cresol red avoids the necessity of using an agarose gel loading buffer. Additionally, glycerol increases the PCR yield.

The PCR mix for a single SSP tube was as follows:

Genomic DNA 100 ng	=	1.00 μ l
<i>Taq</i> polymerase, 0.4 U	=	0.08 μ l
dNTPs, 10 mM	=	0.80 μ l
Buffer, 10x	=	1.00 μ l
Glycerol	=	0.50 μ l
Cresol red 10mg/ml	=	0.10 μ l
dH ₂ O	=	1.52 μ l
Primer Pair + Control		
Primer Pair	=	5.00 μ l
Total		10.00 μ l

The PCR solution was prepared in volumes that would accommodate 30 reactions. The amount of primers used in each 10 μ l PCR volume was 3 pmol of each HLA-A primer and 0.8 pmol of each internal control primer.

The reaction mixture was mixed well, then heated in a Thermo-Cycler 9600 (Perkin-Elmer, Inc) and subjected to the following protocol. After an initial denaturation, a first round with 10 two-temperature cycles was followed by 20 three-temperature cycles.

- 1) Initial denaturation at 95°C for 5 min.
- 2) First 10 cycles
 - i) Denaturation at 95°C for 30 sec.
 - ii) Annealing and extension at 65°C for 50 sec.
- 3) Last 20 cycles
 - i) Denaturation at 95°C for 30 sec.
 - ii) Annealing at 62°C for 50 sec.
 - iii) Extension at 72°C for 30 sec.

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The reaction tube was then cooled on ice. For visualization, 8 ul of the amplification product were run on a 2 % agarose gel prestained with ethidium bromide (0.2 ug/ml). The results were compared to a control lane with known size markers. The reaction products were visualized either as two bands (alleles from different groups) or a single band (alleles from same group). The size of the band(s) were determined and group specificity was assigned according to the length assignments in Table 5.

Figures 10 and 11 show typical gel results, which, as shown in Tables 10 and 11, were interpreted to determine what group specificities were present in genomic DNA samples tested. In Tables 7 and 8, the column titled "Position" refers to the primer mix no. of Table 5.

Table 7.

Position	HLA Specificity	Kontr.	Species ampl.	PM
1	A*0101,0102,8001			1
2	A*0201-0217			2
3	A*0301,0302			3
4	A*0101,3601			36
5	A*1101,1102			11
6	A*2301			23
7	A*2402-2407			24
8	A*2603,2605,6601	X		10.1
9	A*2501			25
10	A*2601,2602,2604,4301			26
11	A*3401,3402			34
12	A*6602			6602
13	A*1101,1102,3401,3402, 6601,6602, A*68011,6802,6901	X		10.2
14	A*4301			43
15	A*68012,6802,6803			68
16	A*6901			69
17	A*2901,2902,3101,3201 3301-3303, A*7401	X		19
18	A*2901,2902			29
19	A*3001-3004			30
20	A*3101			31
21	A*3201,2501	X		32

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Table 8.

Position	HLA Specificity	Kontr. Species	Ampl. PM
1	A*0101,0102,8001		1
2	A*0201-0217	X	2
3	A*0301,0302		3
4	A*0101,3601		36
5	A*1101,1102		11
6	A*2301		23
7	A*2402-2407		24
8	A*2501,2601-2603, 2605,6601		10.1
	A*2501		25
10	A*2601,2602,2604,4301		26
11	A*3401,3402		34
12	A*6602		6602
13	A*1101,1102,3401,3402 6601,6602, A*68011,6802, 6901	X	10.2
14	A*4301		43
15	A*6801,6802	X	68
16	A*6901		69
17	A*2901-2902,3101,3201, 3301-3303, A*7401		19
18	A*2901,2902		29
19	A*3001-3004		30

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7. Example: Determination Of Group Specificity Using A Primer Cocktail

Group specific low-resolution typing of the patient sample may be performed as follows. First, a stock PCR amplification reaction mixture may be prepared for 30 reactions:

	<u>μl</u>
dNTPs 10mM	24
Glycerol 100%	15
10x PCR Buffer*	30
Cresol-red (10mg/ml)	3.0
H ₂ O	<u>45</u>
final	117

*1 X PCR Buffer comprises 10 mM Tris-HCl pH 8.3, 50 mM KCl, 1.5 mM MgCl₂ and 0.001% (w/v) gelatin.

The stock mixture may be prepared in a large volume and be stored for at least one month at 4°C or be aliquoted (117.0 μ l) and stored at -30°C for at least six months. Repeated thawing and freezing should be avoided.

A mixture containing all the HLA-A group specific amplification primers listed in Table 5 may be prepared separately (the "Cocktail"). One member of each primer pair is labelled on the 5' end with a fluorescent label. Final Cocktail concentrations may be designed to provide 3 pmol of each HLA-A primer per 5 μ l. Optionally, an internal control primer may be added (to determine among other things, the success of amplification) in the amount of 0.8 pmol per 5 μ l. Suitable internal control primers amplify a 1074 bp fragment of the human growth hormone gene (see *supra*).

To perform the low resolution amplification reaction, the reaction mixture may be prepared as follows:

	Volume
Stock Mixture	5 μ l
Cocktail	5 μ l
Patient sample DNA 100-250 ng	1 μ l
Taq Polymerase Enzyme 0.4 U	0.08 μ l

PCR cycle parameters may be adjusted for a Perkin-Elmer System 9600 thermal cycler. After an initial denaturation, a first round with 10 two-temperature cycles may be followed by 20 three-temperature cycles: 1) Initial Denaturation at 95°C for 5 min; 2) First 10 cycles i) Denaturation at 95°C for 30 seconds and ii) Annealing and extension at 65°C for 50 seconds; 3) Last 20 cycles i) Denaturation at 95°C for 30 seconds, ii) Annealing at 62°C for 50 seconds and iii) Extension at 72°C for 30 seconds.

The reaction tube may then be cooled on ice. For visualization, 2 μ l of the amplification product may be run on a polyacrylamide gel giving single nucleotide length resolution such as in a MicroGene Blaster. The results were compared to a control lane with known size markers. The reaction products may be visualized either as two bands (alleles from different groups) or a single band (alleles from same group). The size of the band(s) may be determined and group specificity may be assigned according to the length assignments in Table 5.

8. Example: Determination Of Allelic Type By Sequencing

After determining group type specificity, group specific amplification of a fresh portion of the patient sample may be performed using a single pair of primers specific for the group in question to generate sequencing template. In a preferred, nonlimiting embodiment, amplification primers may be selected from Table 2, *supra*, which lists group-specific untranslated region primers. This second amplification serves two purposes. First, it confirms, by successful amplification, the group determination of the low resolution test. Second, it generates sequence information which may be used for accurate allele identification. If two groups are identified, two separate reactions may be performed each using a different primer pair.

8.1. PCR Protocol

The same PCR protocol may be used for all primer mixes used for template generation. The PCR amplification may be set up in a total volume of 50 μ l in order to produce enough PCR product for more than 10 sequencing reactions. This ensures that, if anything fails during the sequencing process, sequencing can be repeated without generation of a new template. The high stringency of the PCR primers and protocol detailed below makes the use of a "hot start approach" unnecessary. The following PCR reaction mix may be used:

	<u>volume per reaction</u>
5X PCR buffer*	10.0 μ l
DMSO	1.0 μ l
2.5mM each dNTP	5.0 μ l
ddH ₂ O	<u>27.8μl</u>
Total	43.8 μ l
Sense primer** (10pmol/ μ l)	1.0 μ l
Antisense primer** (10pmol/ μ l)	1.0 μ l
Taq Polymerase (5U/ μ l)	0.2 μ l
Genomic DNA (100ng/ μ l)	<u>4.0μl</u>
Final Total	50.0 μ l

*Composition of 5X PCR buffer: 75mM (NH₄)₂SO₄; 17.5mM MgCl₂; and 300mM Tris-HCL, pH 9.0

**The pair of group specific amplification primers may be selected from those disclosed in Table 2, *supra*.

PCR cycle parameters may be adjusted for a Perkin-Elmer System 9600 thermal cycler. After an initial denaturation, a first round with 10 two-temperature cycles may be followed by 20 three-temperature cycles.

- 1.) Initial Denaturation at 95 C for 5 min
- 2.) First 10 cycles
 - i) Denaturation at 95 C for 30 seconds
 - ii) Annealing and extension at 65 C for 50 seconds
- 3.) Last 20 cycles
 - i) Denaturation at 95 C for 30 seconds
 - ii) Annealing at 62 C for 50 seconds
 - iii) Extension at 72 C for 30 seconds

10 μ l of the PCR product may then be run on a 2 % agarose gel prestained with ethidium bromide (0,2 μ g/ml). A distinct band of the expected size should be seen.

8.2. Sequencing Reaction Protocol

The sequencing reactions may be carried out with AmpliTaqTM DNA Polymerase FS dye terminator cycle sequencing chemistry using the Ready Reaction DyeDeoxy Terminator Cycle Sequencing Kit FS (Perkin Elmer Applied Biosystems

Division, Foster City, CA) according to the manufacturer's protocol. This Kit contains the four ddNTPs with different fluorescence labels (=Dye Terminators). The PCR fragments may be used directly for sequencing without any prior purification step.

To simplify the pipetting steps, a master mix may be prepared consisting of the 5'Biotin labeled sequencing primer, ddH₂O and the Kit reagents. This master mix should be prepared immediately prior to use and can be kept at room temperature until use. The sequencing master mix for one reaction may comprise 3.0 μ l of a 1pmol/ μ l solution of sequencing primer; 6.0 μ l ddH₂O, and 8.0 μ l of premixed sequencing reagents; for 36 + 1 reactions, these amounts are increased, respectively, to 111.0 μ l; 222.0 μ l; and 296.0 μ l, respectively. The sequencing primer may be selected from the sequencing primers for HLA-A set forth in Table 6, *supra*.

The master mix may be aliquoted in a volume of 17 μ l for each sequencing reaction in a 200 μ l PCR tube and 3 μ l of the unpurified PCR product are added. The reaction mixes may then be subjected to 25 cycles in a Perkin Elmer thermal cycler 9600. Each cycle consists of 10 sec 95 C, 5 sec 50 C and 4 min 60 C.

8.3. Purification Of Extension Products

After the sequencing reaction the extension products are desirably separated from the unincorporated Dye Terminators which would otherwise interfere with the fluorescence-based detection process of the electrophoretically separated sequencing fragments.

For each sequencing reaction, 50 μ g (5 μ l) Streptavidin-coated Dynabeads M-280 (Dynal Inc., Oslo, Norway) may be washed in 5 μ l of 2x Binding and Washing buffer ("B&W"; 2X B&W buffer: 2M NaCl, 10mM Tris-HCl pH 7.5, 1mM EDTA). The beads may then be resuspended in 20 μ l of 2x B&W.

To each 20 μ l sequencing reaction, 20 μ l of resuspended beads may be added, and the mixture may be incubated at room temperature (20-25 C) for 15 minutes. The beads may then be immobilized, the supernatant may be removed, and then the beads may be washed once in 70% ethanol by pipetting up and down five times. Then, as much as possible of the ethanol may desirably be removed, because residual ethanol may interfere with electrophoretic gel mobility.

For each sequencing reaction, 4 μ l of loading buffer (5:1 Formamide-

25mM EDTA pH 8.0, 50mg/ml Dextran Blue) may be added.

8.4. Electrophoresis And Data Collection

Samples prepared by the foregoing methods may be used immediately or be stored at 4 C at least for 24 hours before starting the electrophoretic separation. Prior to the electrophoretic separation, each reaction may be incubated at 90 C for 2 minutes. 3 μ l of each sample may be loaded on a prerun sequencing gel. For an automated ABI 377 sequencer (Applied Biosystems, Foster City, CA) a 0.2mm thick 5% polyacrylamide (acrylamide:bisacrylamide = 29:1) - 7 M urea gel may be used [gel composition: 21.0 g urea, 8.4 ml 30% acrylamide (stock solution: 58g acrylamide, 2g bisacrylamide in bidistilled water), 6.0 ml TBE buffer (10x TBE-buffer: 108.0 g tris base, 55.0 g boric acid, 7.4 g Na₂EDTA), 15 μ l TEMED, 350 μ l 10% Ammoniumpersulfate (1.0 g Ammoniumpersulfate in 10 ml ddH₂O), 20.0 ml ddH₂O]. Electrophoresis may be run at constant 48 watt for 8h. Data collection may be initiated immediately after starting the electrophoresis on the ABI377. Data analyses may be performed thereafter using the ABI analysis software (version 2.1.1).

8.5. Data Interpretation And HLA Typing

After data collection, the chromatograms may be printed and sequences may be compared manually to existing HLA data in the EMBL databank and the sequences compiled by Arnett and Parham. Due to the group-specific amplification and the lack of heterozygous positions, manual analysis is typically very fast. Alternatively, sequences may be checked with the data analysis editor (Sequence NavigatorTM, Applied Biosystems) and aligned with any sequence alignment program.

Various publications are cited herein, the contents of which are hereby incorporated by reference in their entireties.

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT:

(ii) TITLE OF THE INVENTION: Method and Kit for HLA Class
I Typing

(iii) NUMBER OF SEQUENCES: 245

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Baker & Botts, L.L.P.
- (B) STREET: 30 Rockefeller Plaza
- (C) CITY: New York
- (D) STATE: NY
- (E) COUNTRY: U.S.A.
- (F) ZIP: 10112-0228

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: ASCII DOS text
- (D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/766,189
- (B) FILING DATE: 12 DEC 1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Tenser, Arthur and Kole, Lisa
- (B) REGISTRATION NUMBER: 18,839 and 35,225
- (C) REFERENCE/DOCKET NUMBER: 30861

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 212-705-5000
- (B) TELEFAX: 212-705-5020
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele

consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGGTTGCGGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGCATTAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				450

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 0101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGTGCTGTT	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	ACTTCCTGGG	ATGCATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGCTTCGCGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TCCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGTAATAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				450

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 0301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCCGAAATC	TTGTCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	ACTTCCTGGG	ATGCATCCAA	CCCTCTCCCT	CTTTCTTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGAGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGCTTCGCGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TCCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGTAATAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				450

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAGCCCCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTCTCGCTGG	60
CGCTTCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	ACTTCCTGGG	ATGCATCCAA	CCCTCTCCCT	CTTTCTTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGAACA	300
CGCTTCGCGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TCCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGTAATAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				450

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no

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- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A*1102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGCCCCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTCTCGCTGG	60
CGCTTCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCCTACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	ACTTCCTGGG	ATGCATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGAACA	300
CGCTTCGCGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TCCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGTAATAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				450

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCCCGAAATC	TTGTGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCCTACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	ACTTCCTGGG	ATGCATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TCCGACACT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGCTTCGCGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGTAATAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				450

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

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(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCCGAAATC TTGTCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGGTCCT ACTTCCTGGG ATGCATCCAA CCCTCTCCCT CTTTCTTTT      180
ACGCCTCAAC CCCTTAGGGG TTCCGACACT GAGGGGTTAG GTATGTGGCG GAAGCCCCCG      240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGAAGTGGGA GACGAGGACA      300
CGCTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT      360
CCCTCTTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGTAAATAGAG      420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG      450

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCCGAAATC TTGTCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGGTCCT ACTTCCTGGG ATGCATCCAA CCCTCTCCCT CTTTCTTTT      180
ACGCCTCAAC CCCTTAGGGG TTCCGACACT GAGGGGTTAG GTATGTGGCG GAAGCCCCCG      240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGAAGTGGGA GACGAGGACA      300
CGCTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT      360
CCCTCTTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGTAAATAGAG      420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG      450

```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 0201-

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCCTACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCTT	ACTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAAGACA	300
CGGTTCCGGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTGG	GAGCCGTACC	CGGGGCAGGG	AGAGGAAAGT	GAAAAATAGG	GCATTAGAGA	420
CAGGGACTTG	ACCTGAGGGA	CTGAGGGTG				449

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 0215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCCTACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCTT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAAGACA	300
CGGTTCCGGA	GACAGAC	A CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTGG	GAGCCGTACC	CGGGGCAGGG	AGAGGAAAGT	GAAAAATAGG	GCATTAGAGA	420
CAGGGACITG	ACCTGAGGGA	CTGAGGGTG				449

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 0217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAAGACA	300
CGGTTGCGGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTGG	GAGCCGTACC	CGGGGCAGGG	AGAGGAAAGT	GAAAAATAGG	GCATTAGAGA	420
CAGGGACTTG	ACCTGAGGGA	CTGAGGGTG				449

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGGTTGCGGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTA	360
CCCTCTTTGG	GAGCCGTACC	CGGGGCAGGG	AGAGGAAAGT	GAAAAATAGG	GCATTAGAGA	420
CAGGGACTTG	ACCTGAGGGA	CTGAGGGTG				449

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

SUBSTITUTE SHEET (rule 26)

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GAGCCGCAGA	CCCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGGTTGCGGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTA	360
CCCTCTTTGG	GAGCCGTACC	CGGGGCAGGG	AGAGGAAAGT	GAAAAATAGG	GCATTAGAGA	420
CAGGGACTTG	ACCTGAGGGA	CTGAGGGTG				449

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAGCCGCAGA	CCCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGGTTGCGGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTA	360
CCCTCTTTGG	GAGCCGTACC	CGGGGCAGGG	AGAGGAAAGT	GAAAAATAGG	GCATTAGAGA	420
CAGGGACTTG	ACCTGAGGGA	CTGAGGGTG				449

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGCCGCAGA	CCCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGTGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120

SUBSTITUTE SHEET (rule 26)

GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCCG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAAGACA	300
CGGTTTCGCGA	GACAGAGTTA	CAGAGGGACT	TAGAACC GGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGCATTAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				450

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGTGCGTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCCG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAAGACA	300
CGGTTTCGCGA	GACAGAGTTA	CAGAGGGACT	TAGAACC GGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGCATTAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				450

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGTGCGTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCCG	240

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ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAAGACA	300
CGGTTCCGGA	GACAGAGTTA	CAGAGGGACT	TAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGCATTAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				450

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGTCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGTCTCT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAAGACA	300
CGGTTCCGGA	GACAGAGTTA	CAGAGGGACT	TAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGCATTAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				450

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGTCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGTCTCT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAAGACA	300
CGGTTCCGGA	GACAGAGTTA	CAGAGGGACT	TAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360

SUBSTITUTE SHEET (rule 26)

CCCTCTTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG 420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG 450

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGTCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCCTACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAAGACA	300
CGGTTGCGGA	GACAGAGTTA	CAGAGGGACT	TAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGCATTAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				450

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCCTACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCGTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGGTTGCGGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTTG	GGAGCCGTAC	CCGGGGCAGG	GAGAGGAAAG	TGAAAAGTAG	GGCATTAGAG	420
ACAGGGACTT	GACCTGAGGG	ACTGAGGGTG				445

SUBSTITUTE SHEET (rule 26)

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCTGAAATC TTGGCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGTCCTT TCTTCTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG      180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCT GAGGGGTTAG GTATATGGCG GAAGCCCCGG      240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGAAGGGGGA GACGAGGACA      300
CGGTTTCGGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT      360
CCCTCTTTTG GGAGCCGTAC CCGGGCAGG GAGAGGAAAG TGAAAAATAG GGCATTAGAG      420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG      450

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCTGAAATC TTGGCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGTCCTT TCTTCTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG      180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG      240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGAAGGGGGA GACGAGGACA      300
CGGTTTCGGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT      360
CCCTCTTTTG GAGCCGTACC CCGGGCAGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA      420
CAGGGACTTG ACCTGAGGGA CTGAGGGTG      449

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(2) INFORMATION FOR SEQ ID NO:24:

SUBSTITUTE SHEET (rule 26)

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 4301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

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GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCTGAAATC TTGGCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGGTCCT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG      180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCT GAGGGGTTAG GTATATGGCG GAAGCCCCGG      240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA      300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT      360
CCCTCTTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA      420
CAGGGACTTG ACCTGAGGGA CTGAGGGTG      449

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(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCTGAAATC TTGGCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGGTCCT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG      180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG      240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA      300
CGGTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT      360
CCCTCTTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAATAGG GCATTAGAGA      420
CAGGGACTTG ACCTGAGGGA CTGAGGGTG      449

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(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATTCGCAGA	CCCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGGTTGCGGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTA	360
CCCTCTTTGG	GAGCCGTACC	CGGGGCAGGG	AGAGGAAAGT	GAAAAATAGG	GCATTAGAGA	420
CAGGGACTTG	ACCTGAGGGA	CTGAGGGTG				449

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 6603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGCCGCAGA	CCCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCCTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCGG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGGTTGCGGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTA	360
CCCTCTTTGG	GAGCCGTACC	CGGGGCAGGG	AGAGGAAAGT	GAAAAATAGG	GCATTAGAGA	420
CAGGGACTTG	ACCTGAGGGA	CTGAGGGTG				449

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCCT TCTTCCTGGG ATGTATCCAA CCGTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGAGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 2902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCACGCAC GCCTGAAATC TTGGCGCTGG	60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG	120
GCGCAGCACT CATAGGTCCT TCTTCCTGGG ATGTATCCAA CCGTCTCCCT CTTTTCTTTG	180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG	240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA	300
CGGTTCGAGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT	360
CCCTCTTTTG GGAGCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG	420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG	450

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

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- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 31012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCTGAAATC TTGGCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGGTCCT TCTTCCTGGG ATGTATCCAA CCTCTCCCT CTTTCTTTG      180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCCG      240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCATGAAGCG GGACTGGGGA GACGAGGACA      300
CGGTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT      360
CCCTCTTTTG GGACCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG      420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG                                     450

```

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCTGAAATC TTGGCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGGTCCT TCTTCCTGGG ATGTATCCAA CCGTCTCCCT CTTTCTTTG      180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCCG      240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA      300
CGGTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT      360
CCCTCTTTTG GAGCCGTACC CCGGGCAGGG AGAGGAAAGT GAAAAGTAGG GCATTAGAGA      420
CAGGGACTTG ACCTGAGGGA CTGAGGGTG                                     449

```

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no

- (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
- (ix) FEATURE:
 (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCTGAAATC TTGGCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGGTCCT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG      180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCCG      240
ACTCTGGGAC TCTCGGTGCG GACCCCGGA CCATGAAGCG GGACTGGGGA GACGAGGACA      300
CGGTTCCGGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT      360
CCCTCTTTTG GGACCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG      420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG      450

```

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 3303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCTGAAATC TTGGCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGGTCCT TCTTCCTGGG ATGTATCCAA CCCTCTCCCT CTTTCTTTG      180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCCG      240
ACTCTGGGAC TCTCGGTGCG GACCCCGGA CCATGAAGCG GGACTGGGGA GACGAGGACA      300
CGGTTCCGGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TTCTCGACAG ACTCTTTGTT      360
CCCTCTTTTG GGACCCGTAC CCGGGGCAGG GAGAGGAAAG TGAAAAGTAG GGCATTAGAG      420
ACAGGGACTT GACCTGAGGG ACTGAGGGTG      450

```

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

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(ix) FEATURE:

(A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 7401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCTGAAATC TTGGCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGGTCCT TCTTCCTGGG ATGTATCCAA CCGTCTCCCT CTTTTCTTTG      180
ACGCCTCAAC CCCTTAGGGG TTCCGACCCT GAGGGGTTAG GTATGTGGCG GAAGCCCCGG      240
ACTCTGGGAC TCTCGGTGCG GACCCCGGGA CCCTGAAGCG GGACTGGGGA GACGAGGACA      300
CGGTTGCGGA GACAGAGTTA CAGAGGGACT CAGAACCGG TTCTCGACAG ACTCTTTGTT      360
CCCTCTTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAGTAGG GCATTAGAGA      420
CAGGGACTTG ACCTGAGGGA CTGAGGGTG      449

```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: IL-210m

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

ACCCGGGAAG CCGGGCCT      18

```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 7402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

GAGCCGCAGA CCCCTCTTAG ACTCAGGGCC ACCCAGGCAC GCCTGAAATC TTGGCGCTGG      60
CGCTGCTGTG ACTAACCGAA GAGACCTTTG GGCTGTGGGT TACCCTCACT CTTGACCCAG      120
GCGCAGCACT CATAGGTCCT TCTTCCTGGG ATGTATCCAA CCGTCTCCCT CTTTTCTTTG      180

```

ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCCG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGGTTCCGGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTGG	GAGCCGTACC	CGGGGCAGGG	AGAGGAAAGT	GAAAAGTAGG	GCATTAGAGA	420
CAGGGACTTG	ACCTGAGGGA	CTGAGGGTG				449

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 7403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TACCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCGTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGGGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCCG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300
CGGTTCCGGA	GACAGAGTTA	CAGAGGGACT	CAGAACCGGG	TTCTCGACAG	ACTCTTTGTT	360
CCCTCTTTGG	GAGCCGTACC	CGGGGCAGGG	AGAGGAAAGT	GAAAAGTAGG	GCATTAGAGA	420
CAGGGACTTG	ACCTGAGGGA	CTGAGGGTG				449

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Flanking Region Allele A* 8001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAGCCGCAGA	CCCCTCTTAG	ACTCAGGGCC	ACCCACGCAC	GCCTGAAATC	TTGGCGCTGG	60
CGCTGCTGTG	ACTAACCGAA	GAGACCTTTG	GGCTGTGGGT	TATCCTCACT	CTTGACCCAG	120
GCGCAGCACT	CATAGGTCCT	TCTTCCTGGG	ATGTATCCAA	CCGTCTCCCT	CTTTTCTTTG	180
ACGCCTCAAC	CCCTTAGAGG	TTCCGACCCT	GAGGGGTTAG	GTATGTGGCG	GAAGCCCCCG	240
ACTCTGGGAC	TCTCGGTGCG	GACCCCGGGA	CCCTGAAGCG	GGACTGGGGA	GACGAGGACA	300

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CGCTTCGCGA GACAGAGTTA CAGAGGGACT CAGAACCGGG TCCTCGACAG ACTCTTTGTT 360
CCCTCTTTGG GAGCCGTACC CGGGGCAGGG AGAGGAAAGT GAAAAGTAGG GCATTAGAGA 420
CAGGGACTTG ACCTGAGGGA CTGAGGGTG 449

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTGAGTGCGG GGTCCGGGAGG GAAACGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCTGGC 60
GGGGGCGCAG GACCCGGGAA GCCGCGCCGG GAGGAGGGTC GGGCAGGTCT CAGCCACTCC 120
TCGCCCCCAG 130

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A 5' Intron Allele A* 0101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGAGTGCGG GGTCCGGGAGG GAAACGCCT CTGCGGGGAG AAGCAAGGGG CCCTCCTGGC 60
GGGGGCGCAG GACCCGGGGA GCCGCGCCGG GAGGAGGGTC GGGCAGGTCT CAGCCACTGC 120
TCGCCCCCAG 130

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```
GTGAGTGCGG GGTCTGGGAGG GAAACCGCCT CTGCGGGGAG AAGCAAGGGG CCCTCCTGGC 60
GGGGGCGCAG GACCGGGGGA GCCGCGCCGG GACGAGGGTC GGGCAGGTCT CAGCCACTGC 120
TCGCCCCCAG 130
```

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
GTGAGTGCGG GGTCTGGGAGG GAAACCGCCT CTGCGGGGAG AAGCAAGGGG CCCTCCTGGC 60
GGGGGCGCAG GACCGGGGGA GCCGCGCCGG GAGGAGGGTC GGGCAGGTCT CAGCCACTGC 120
TCGCCCCCAG 130
```

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 1102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
GTGAGTGCGG GGTCTGGGAGG GAAACCGCCT CTGCGGGGAG AAGCAAGGGG CCCTCCTGGC 60
GGGGGCGCAG GACCGGGGGA GCCGCGCCGG GAGGAGGGTC GGGCAGGTCT CAGCCACTGC 120
```

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TCGCCCCCAG

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
GTGAGTGCGG GGTCTGGGAGG GAAACCGCCT CTGCGGGGAG AAGCAAGGGG CCCTCCTGGC 60
GGGGGCGCAG GACCGGGGGA GCCGCGCCGG GAGGAGGGTC GGTCAGGTCT CAGCCACTGC 120
TCGCCCCCAG 130
```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```
GTGAGTGCGG GGTCTGGGAGG GAAACCGCCT CTGCGGGGAG AAGCAAGGGG CCCTCCTGGC 60
GGGGGCGCAG GACCGGGGGA GCCGCGCCGG GAGGAGGGTC GGTCAGGTCT CAGCCACTGC 120
TCGCCCCCAG 130
```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no

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- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

GTGAGTGC GGTCGGGAGG GAAACCGCCT CTGCGGGGAG AAGCAAGGGG CCCTCCTGGC    60
GGGGCGCAG GACCGGGGA GCCGCGCCGG GAGGAGGGTC GGTGAGGTCT CAGCCACTGC    120
TCGCCCCCAG                                     130

```

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAACGGG CCGCCTGGCG    60
GGGGCGCAG ACCCGGAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT    120
CGTCCCCAG                                     129

```

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAACGGG CCGCCTGGCG    60
GGGGCGCAG ACCCGGAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT    120
CGTCCCCAG                                     129

```

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(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTGAGTGC	GGTCTGGG	GAGG	GAAACGGC	CTGTGGGG	AAGCAACGGG	CCGCCTGGCG	60
GGGGCGCAGG	ACCCGGAAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGGTCTC	AGCCACTCCT		120
CGTCCCCAG							129

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTGAGTGC	GGTCTGGG	GAGG	GAAACGGC	CTGTGGGG	AAGCAACGGG	CCGCCTGGCG	60
GGGGCGCAGG	ACCCGGAAG	CCGCGCCGGG	AGGAGGGTCG	GGCGGGTCTC	AGCCACTCCT		120
CGTCCCCAG							129

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

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(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 1 Allele A* 0205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
GTGAGTGGCG GGTCTGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAACGGG CCGCCTGGCG      60
GGGGCGCAGG ACCCGGGAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT      120
CGTCCCCAG                                     129
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 1 Allele A* 0206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
GTGAGTGGCG GGTCTGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAACGGG CCGCCTGGCG      60
GGGGCGCAGG ACCCGGGAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT      120
CGTCCCCAG                                     129
```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 1 Allele A* 0207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```
GTGAGTGGCG GGTCTGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAACGGG CCGCCTGGCG      60
GGGGCGCAGG ACCCGGGAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT      120
CGTCCCCAG                                     129
```

(2) INFORMATION FOR SEQ ID NO:54:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGTGGGAG AAGCAACGGG CCGCCTGGCG      60
GGGGCGCAGG ACCCGGAAG CCGCGCCGGG AGGAGGGTCG GCGGGGTCTC AGCCACTCCT      120
CGTCCCCAG                                     129
```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGTGGGAG AAGCAACGGG CCGCCTGGCG      60
GGGGCGCAGG ACCCGGAAG CCGCGCCGGG AGGAGGGTCG GCGGGGTCTC AGCCACTCCT      120
CGTCCCCAG                                     129
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0209

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAACGGG CCGCCTGGCG    60
GGGGCGCAGG ACCCGGGAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT    120
CGTCCCCAG                                     129
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAACGGG CCGCCTGGCG    60
GGGGCGCAGG ACCCGGGAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT    120
CGTCCCCAG                                     129
```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAACGGG CCGCCTGGCG    60
GGGGCGCAGG ACCCGGGAAG CCGCGCCGGG AGGAGGGTCG GGCGGGTCTC AGCCACTCCT    120
CGTCCCCAG                                     129
```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GTGAGTGC	GG	GGT	CGG	GAGG	GAA	ACG	GCCT	CTGT	GGG	GAG	AAG	CAAC	GGG	CCG	CCT	GGCG	60
GGGGCG	CAGG	ACCC	GGGA	AG	CCG	CCCG	GG	AGG	AGG	GTCG	GGC	GGGT	CCTC	AGC	CACT	CTCT	120
CGT	CCCC	CAG															129

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 0217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GTGAGTGC	GG	GGT	CGG	GAGG	GAA	ACG	GCCT	CTGT	GGG	GAG	AAG	CAAC	GGG	CCG	CCT	GGCG	60
GGGGCG	CAGG	ACCC	GGGA	AG	CCG	CCCG	GG	AGG	AGG	GTCG	GGC	GGGT	CCTC	AGC	CACT	CTCT	120
CGT	CCCC	CAG															129

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 6801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

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```

GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCCCGGC 60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
TCGCCCCCAG 130

```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 6802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCCCGGC 60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
TCGCCCCCAG 130

```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 6901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCCCGGC 60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
TCGCCCCCAG 130

```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

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- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

GTGAGTGCGG GGTCTGGGAGG GAAACGGCCT CTGCGGGGAG AAGCAAGGGG CCCGCCTGGC    60
GGGGGCGCAA GACCCGGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC    120
TCGTCCCCAG                                     130

```

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

GTGAGTGCGG GGTCTGGGAGG GAAACGGCCT CTGCGGGGAG AAGCAAGGGG CCCGCCTGGC    60
GGGGGCGCAA GACCCGGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC    120
TCGTCCCCAG                                     130

```

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

GTGAGTGCGG GGTCTGGGAGG GAAACGGCCT CTGCGGGGAG AAGCAAGGGG CCCGCCTGGC    60
GGGGGCGCAA GACCCGGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC    120

```

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TCGTCCCCAG

130

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGCGGGGAG AAGCAAGGGG CCCGCCTGGC 60
GGGGGCGCAA GACCCGGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
TCGTCCCCAG 130
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGCGGGGAG AAGCAAGGGG CCCGCCTGGC 60
GGGGGCGCAA GACCCGGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
TCGTCCCCAG 130
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no

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- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

GTGAGTGCGG GGTCTGGGAGG GAAACGGCCT CTGCGGGGAG AAGCAAGGGG CCGCCTGGC    60
GGGGGCGCAA GACCCGGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC    120
TCGTCCCCAG                                     130

```

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

GTGAGTGCGG GGTCTGGGGG AAACCGCCTC TCGGGGGAGA AGCAAGGGGC CCGCCCGGCG    60
GGGACGCAGG ACCCGGGTAG CCGCGCCGGG AGGAGGGTCG GGTGGGTCTC AGCCACTCCT    120
CGCCCCCAG                                     129

```

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

GTGAGTGCGG GGTCTGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCGCCCCGGC    60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC    120
TCGCCCCCAG                                     130

```

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(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```
GTGAGTGC GG GGTCTGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCCCGGC 60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
TCGCCCCCAG 130
```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 6601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
GTGAGTGC GG GGTCTGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCCCGGC 60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
TCGCCCCCAG 130
```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

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(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 1 Allele A* 6602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
GTGAGTGCGG GGTCTGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCCCGGC 60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
TCGCCCCCAG 130
```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 1 Allele A* 6603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
GTGAGTGCGG GGTCTGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCCCGGC 60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
TCGCCCCCAG 130
```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 1 Allele A* 4301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```
GTGAGTGCGG GGTCTGGGAGG GAAACGGCCT CTGTGGGGAG AAGCAAGGGG CCCGCCCCGGC 60
GGGGGCGCAG GACCCGGGAA GCCGCGCCTG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
TCGCCCCCAG 130
```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```
GTGAGTGCGG GGTCTGTTGGG AAACCGCCTC TCGGGGAGAG AGCAAGGGGC CCGCCCGGCG      60
GGGACGCAGG ACCCGGGTAG CCGCGCCGGG AGGAGGGTCG GGTGGGTCTC AGCCACTCCT      120
CGCCCCCAG                                     129
```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 2902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```
GTGAGTGCGG GGTCTGTTGGG AAACCGCCTC TCGGGGAGAG AGCAAGGGGC CCGCCCGGCG      60
GGGACGCAGG ACCCGGGTAG CCGCGCCGGG AGGAGGGTCG GGTGGGTCTC AGCCACTCCT      120
CGCCCCCAG                                     129
```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3101

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GTGAGTGC	GGT	CGT	G	GGG	AAAC	CGC	CTC	TGCG	GGG	GAGA	AGCA	AGG	GGC	CCG	CCCG	GGCG	60	
GGGG	CGC	CAGG	ACCC	GGGT	AG	CCG	CGC	CGG	AGG	AGG	GTCG	GGC	GGAT	CTC	AGCC	ACTC	CT	120
CGCCCC	CAG																	129

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GTGAGTGC	GGT	CGT	G	GGG	AAAC	CGC	CTC	TGCG	GGG	GAGA	AGCA	AGG	GGC	CCG	CCCG	GGCG	60	
GGGG	CGC	CAGG	ACCC	GGGT	AG	CCG	CGC	CGG	AGG	AGG	GTCG	GGC	GGAT	CTC	AGCC	ACTC	CT	120
CGCCCC	CAG																	129

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GTGAGTGC	GGT	CGT	G	GGG	AAAC	CGC	CTC	TGCG	GGG	GAGA	AGCA	AGG	GGC	CCG	CCCG	GGCG	60	
GGGG	CGC	CAGG	ACCC	GGGT	AG	CCG	CGC	CGG	AGG	AGG	GTCG	GGC	GGAT	CTC	AGCC	ACTC	CT	120
CGCCCC	CAG																	129

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 3303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
GTGAGTGCGG GGTCTGTGGG AAACCGCCTC TCGGGGAGA AGCAAGGGGC CCGCCCGCG 60
GGGGCGCAGG ACCCGGTAG CCGCGCCGGG AGGAGGGTCG GCGGATCTC AGCCACTCCT 120
CGCCCCCAG 129
```

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 7401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```
GTGAGTGCGG GGTCTGTGGG AAACCGCCTC TCGGGGAGA AGCAAGGGGC CCGCCCGCG 60
GGGGCGCAGG ACCCGGTAG CCGCGCCGGG AGGAGGGTCG GCGGGTCTC AGCCACTCCT 120
CGCCCCCAG 129
```

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 7402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

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GTGAGTGC GGTCGTGGGG AAACCGCCTC TCGGGGGAGA AGCAAGGGGC CCGCCCCGGC 60
GGGGCGCAGG ACCCGGGTAG CCGCGCCGGG AGGAGGGTCG GCGGGGTCTC AGCCACTCCT 120
CGCCCCCAG 129

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 7403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGAGTGC GGTCGTGGGG AAACCGCCTC TCGGGGGAGA AGCAAGGGGC TCGCCCCGGC 60
GGGGCGCAGG ACCCGGGTAG CCGCGCCGGG AGGAGGGTCG GCGGGGTCTC AGCCACTCCT 120
CGCCCCCAG 129

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 1 Allele A* 8001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GTGAGTGC GGTCGGGAGG GAAACGGCCT CTGCGGGGAG AAGCAAGGGG CCGCCCCGGC 60
GGGGCGCAG GACCCGGGAA GCCGCGCCGG GAGGAGGGTC GGGCGGGTCT CAGCCACTCC 120
TCGCCCCCAG 130

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

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- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA      240
G

```

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACTCCG AGACCCTTGT      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA      240
G

```

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0201

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTGAGTGACC	CCGGCCCGGG	GCGCAGGTCA	CGACCTCTCA	TCCCCCACGG	ACGGGCCCAGG	60
TCGCCCACAG	TCTCCGGGTC	CGAGATCCGC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCAGGTTGGT	CGGGGCGGGG	CGGGGCTCGG	GGGACCGGGC	TGACCGCGGG	GTCCGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron Allele A* 0202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GTGAGTGACC	CCGGCCCGGG	GCGCAGGTCA	CGACCTCTCA	TCCCCCACGG	ACGGGCCCAGG	60
TCGCCCACAG	TCTCCGGGTC	CGAGATCCGC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCAGGTTGGT	CGGGGCGGGG	CGGGGCTCGG	GGGACCGGGC	TGACCGCGGG	GTCCGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron Allele A* 0203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GTGAGTGACC	CCGGCCCGGG	GCGCAGGTCA	CGACCTCTCA	TCCCCCACGG	ACGGGCCCAGG	60
TCGCCCACAG	TCTCCGGGTC	CGAGATCCGC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCAGGTTGGT	CGGGGCGGGG	CGGGGCTCGG	GGGACCGGGC	TGACCGCGGG	GTCCGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG    60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC    120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC    180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGGCCA    240
G                                                                    241
```

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG    60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC    120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC    180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGGCCA    240
G                                                                    241
```

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

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- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA      240
G                                                                                   241

```

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA      240
G                                                                                   241

```

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTGAGTGACC	CCGGCCCCGGG	GCGCAGGTCA	CGACCTCTCA	TCCCCACGG	ACGGGCCAGG	60
TCGCCCCACAG	TCTCCGGGTC	CGAGATCCGC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCAGGTTGGT	CGGGGCGGGG	CGGGGCTCGG	GGGACCGGGC	TGACCGCGGG	GTCCGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTGAGTGACC	CCGGCCCCGGG	GCGCAGGTCA	CGACCTCTCA	TCCCCACGG	ACGGGCCAGG	60
TCGCCCCACAG	TCTCCGGGTC	CGAGATCCGC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCAGGTTGGT	CGGGGCGGGG	CGGGGCTCGG	GGGACCGGGC	TGACCGCGGG	GTCCGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGAGTGACC	CCGGCCCCGGG	GCGCAGGTCA	CGACCTCTCA	TCCCCACGG	ACGGGCCAGG	60
TCGCCCCACAG	TCTCCGGGTC	CGAGATCCGC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCAGGTTGGT	CGGGGCGGGG	CGGGGCTCGG	GGGACCGGGC	TGACCGCGGG	GTCCGGGCCA	240
G						241

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(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA      240
G                                                                                   241

```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron Allele A* 0215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA      240
G                                                                                   241

```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

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- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```
GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCAGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCGCGGG GTCCGGGCCA      240
G
```

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 6801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```
GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA      240
G
```

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 6802

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GTGAGTGACC	CCGGCCCGGG	GCGCAGGTCA	CGACCCCTCA	TCCCCACGG	ACGGGCCAGG	60
TCGCCCACAG	TCTCCGGGTC	CGAGATCCGC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCGGGTTGGT	CGGGGCGGGG	CGGGGCTCGG	GGGACCGGGC	TGACCTCGGG	GTCCGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 6901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GTGAGTGACC	CCGGCCCGGG	GCGCAGGTCA	CGACCTCTCA	TCCCCACGG	ACGGGCCAGG	60
TCGCCCACAG	TCTCCGGGTC	CGAGATCCGC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCAGGTTGGT	CGGGGCGGGG	CGGGGCTCGG	GGGACCGGGC	TGACCGCGGG	GTCCGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGAGTGACC	CCGGCCCGGG	GCGCAGGTCA	CGACCCCTCA	TCCCCACGG	ACGGGCCAGG	60
TCGCCCACAG	TCTCCGGGTC	CGAGATCCGC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCGGGTTGGT	CGGGGCGGGG	CGGGGCTCGG	GGGACCGGGC	TGACCTCGGG	GTCCGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGSCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA      240
G                                          241

```

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 4301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGSCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA      240
G                                          241

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

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- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 6601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 6602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCAGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCGC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCGGGG CGGGGCTCGG GGGACCGGGC TGACCTCGGG GTCCGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 660

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTGAGTGACC	CCGSCCCGGG	GCGCAGGTCA	CGACCCCTCA	TCCCCCACGG	ACGGGCCAGG	60
TCGCCCACAG	TCTCCGGGTC	CGAGATCCGC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCGGGTTGGT	CGGGCCGGG	CGGGGCTCGG	GGGACCGGGC	TGACCTCGGG	GTCCGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GTGAGTGACC	CCGGCCCCGGG	GCGCAGGTCA	CGACCTCTCA	TCCCCCACGG	ACGGGCCGGG	60
TCGCCCACAG	TCTCCGGGTC	CGAGATCCAC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCGGGTTGGT	CGGGGCCGGG	CGGGGCTCGG	GGGACCGGGC	TGACCTCGGG	GTCCGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GTGAGTGACC	CCGGCCCCGGG	GCGCAGGTCA	CGACCTCTCA	TCCCCCACGG	ACGGGCCGGG	60
TCGCCCACAG	TCTCCGGGTC	CGAGATCCAC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGC	120
CCCGGGAGAG	GCCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATCCCC	180
CCGGGTTGGT	CGGGGCCGGA	CGGGGCTCGG	GGGACTGGGC	TGACCGTGGG	GTCCGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCGGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA      240
G

```

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```

GTGAGTGACC CCAGCCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG      60
TCACCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA      240
G

```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA      240
G

```

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

GTGAGTGACC CCAGCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG      60
TCACCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA      240
G

```

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3303

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```

GTGAGTGACC CCAGCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG 60
TCACCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC 120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC 180
CCGGGTTGGT CGGGGCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA 240
G 241

```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 7401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA GGACCCCTCA TCCCCACGG ACGGGCCAGG 60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC 120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC 180
CCGGGTTGGT CGGGGCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA 240
G 241

```

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 7402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCTCTCA TCCCCACGG ACGGGCCAGG 60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC 120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC 180
CCGGGTTGGT CGGGGCCGGA CGGGGCTCGG GGGACTGGGC TGACCGTGGG GTCGGGGCCA 240
G 241

```

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 7403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA GGACCCCTCA TCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCAATTTT AGTTTAGGCC AAAAATCCCC      180
CCGGGTGGT  CCGGGCCGGA CGGGGCTCGG GGGACTGGG TGACCGTGG GTCGGGGCCA      240
G

```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCGGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTAACCCGG TTTCAATTTT AGTTTAGGCC AAAAATCCCC      180
CCGGGTGGT  CCGGGCCGGA CGGGGCTCGG GGGACTGGG TGACCGCGGG GTCGGGGCCA      240
G

```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

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- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCGGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTAACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCGGG	60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC	120
CCCGGGAGAG GCCCAGGCGC CTTAACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC	180
CCGGGTTGGT CGGGGCCGGG GGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2404

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCGGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTAACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA      240
G

```

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCGGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTAACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA      240
G

```

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```

GTGAGTGACC CCGGCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCGGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCTTGC      120
CCCGGGAGAG GCCCAGGCGC CTTAACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCCGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA      240
G

```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 0301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA GGACCCCTCA TCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCCTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTTATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCTGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA      240
G                                                                                   241

```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA CGACCCCTCA TCCCCACGG ACGGGCCAGG      60
TGGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCCTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTTATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCCGGG CAGGGCTTGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA      240
G                                                                                   241

```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 1102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```

GTGAGTGACC CCGGCCCCGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG      60
TGGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCCTGC      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCCGGG CAGGGCTTGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA      240
G                                                                           241

```

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```

GTGAGTGACC CCGGCCGGGG GCGCAGGTCA CGACCCCTCA TCCCCCACGG ACGGGCCAGG      60
TCGCCCACAG TCTCCGGGTC CGAGATCCAC CCCGAAGCCG CGGGACCCCG AGACCCCTGA      120
CCCGGGAGAG GCCCAGGCGC CTTTACCCGG TTTCATTTTC AGTTTAGGCC AAAAATCCCC      180
CCGGGTTGGT CGGGGCTGGG CGGGGCTCGG GGGACTGGGC TGACCGCGGG GTCGGGGCCA      240
G                                                                           241

```

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GTGAGTGACC	CCGCCCCGGG	GCGCAGGTCA	CGACCCCTCA	TCCCCCACGG	ACGGGCCCAGG	60
TCGCCCCACAG	TCTCCGGGTC	CGAGATCCAC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGA	120
CCCGGGAGAG	GCCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATTCCC	180
CCGGGTTGGT	CGGGGCTGGG	CGGGGCTCGG	GGGACTGGGC	TGACCGCGGG	GTCGGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 3004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GTGAGTGACC	CCGGCCGGGG	GCGCAGGTCA	CGACCCCTCA	TCCCCCACGG	ACGGGCCCAGG	60
TCGCCCCACAG	TCTCCGGGTC	CGAGATCCAC	CCCGAAGCCG	CGGGACCCCG	AGACCCTTGA	120
CCCGGGAGAG	GCCCAGGCGC	CTTTACCCGG	TTTCATTTTC	AGTTTAGGCC	AAAAATTCCC	180
CCGGGTTGGT	CGGGGCTGGG	CGGGGCTCGG	GGGACTGGGC	TGACCGCGGG	GTCGGGGCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 2 Allele A* 8001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GTGAGTGACC	CCGGCCCCGG	GCGCAGGTCA	GACCCCTCAT	CCCCTACGGA	CGGGCCAGGT	60
CGCCCCACAGT	CTCCGGGTCC	GAGATCCACC	CCGAAGCCGC	GGGACCCCGA	GACCCTTGCC	120
CCGGGAGAGG	CCCAGGCGCC	TTTAGCCGGT	TTTCATTTTC	GTTTAGGCCA	AAAAATCCCC	180
CGGGTGGGTC	GGGGCGGGGC	GGGGCTCGGG	GGACCGGGCT	GACCGCGGGG	TCGGGGCCAG	240

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCTTC TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAAT CTCTGAAGGA ATGACGGGAA GACGATCCCT    240
CGAATACTGA TGAGTGGTTC CCTTTGACAC ACACCGGCAG CAGCCTTGGG CCCGTGACTT    300
TTCCTCTCAG GCCTTGTTC CTGCTTCACA CTCATGTGT GTGGGGGTCT GAGTCCAGCA    360
CTTCTGAGTC CCTCAGCCTC CACTCAGGTC AGGACCAGAA GTCGCTGTTC CCTCTTCAGG    420
GACTAGAATT TTCCACGGAA TAGGAGATTA TCCCAGGTGC CTGTGTCCAG GCTGGTGTCT    480
GGGTCTGTG TCCCTTCCC CATCCCAGGT GTCCTGTCCA TTCTCAAGAT AGCCACATGT    540
GTGCTGGAGG AGTGTCCCAT GACAGATGCA AAATGCCTGA ATGTTCTGAC TCTTCCTGAC    600
AG

```

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTATAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAG TGACGGGAAG ACGATCCCTC    240
GAATACTGAT GAGTGGTTCC CTTTGACACC GGCAGCAGCC TTGGGCCCCG GACTTTTCCT    300
CTCAGGCCTT GTTCTCTGCT TCACACTCAA TGTGTGTGGG GGTCTGAGTC CAGCACTTCT    360
GAGTCTCTCA GCCTCCACTC AGGTCCAGGAC CAGAAGTCGC TGTTCCCTTC TCAGGGATA    420
GAAGATTATC CCAGGTGCCT GTGTCCAGGC TGGTGTCTGG GTTCTGTGCT CTCTCCCCA    480

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97

TCCCGGGTGT CCTGTCCATT CTCAAGATGG CCACATGCGT GCTGGTGGAG TGTCCCATGA 540
 CAGATGCAAA ATGCCTGAAT TTTCTGACTC TTCCCGTCAG 580

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA 60
 CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCCTGAGGG 120
 AGAGGAATCC TCCTGGGTTT CAGATCCTGT ACCAGAGAGT GACTCTGAGG TTCCGCCCTG 180
 CTCTCTGAGC ACAATTAAGG GATAAAATCT CTGAAGGAGT GACGGGAAGA CGATCCCTCG 240
 AATACTGATG AGTGGTTCCC TTGACACCG GCAGCAGCCT TGGGCCCCGTG ACTTTTCCTC 300
 TCAGGCCTTG TTCTCTGCTT CACACTCAAT GTGTGTGGGG GTCTGAGTCC AGCACTTCTG 360
 AGTCCCTCAG CCTCCACTCA GGTGAGGACC AGAAGTCGCT GTTCCCTTCT CAGGGAATAG 420
 AAGATTATCC CAGGTGCCTG TGTCCAGGCT GGTGTCTGGG TTCTGTGCTC TCTTCCCAT 480
 CCCGGGTGTC CTGTCCATTC TCAAGATGGC CACATGCGTG CTGGTGGAGT GTCCCATGAC 540
 AGATGCAAAA TGCCTGAATT TTCTGACTCT TCCCGTCAG 579

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTATAGA TCTCCCGGGC TGGCCTCCCA 60
 CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCCTGAGGG 120
 AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGAATCTGAG GTTCCGCCCT 180
 GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAG TGACGGGAAG ACGATCCCTC 240
 GAATACTGAT GAGTGGTTTC CTTTGACACC GGCAGCAGCC TTGGGCCCCG GACTTTTCCT 300
 CTCAGGCCTT GTTCTCTGCT TCACACTCAA TGTGTGTGGG GGTCTGAGTC CAGCACTTCT 360

SUBSTITUTE SHEET (rule 26)

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GAGTCTCTCA	GCCTCCACTC	AGGTCAGGAC	CAGAAGTCGC	TGTTCCCTTC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCGGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCGT	GCTGGTGGAG	TGTCCCATGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 1102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTATAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCAC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAG	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGCCCCG	GACTTTTCCT	300
CTCAGGCCTT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCTCTCA	GCCTCCACTC	AGGTCAGGAC	CAGAAGTCGC	TGTTCCCTTC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCGGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCGT	GCTGGTGGAG	TGTCCCATGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GTACCAGGGG	CCACGGGGCG	CCTTCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCAC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAG	TGACGGGAAG	ACGATCCCTC	240

SUBSTITUTE SHEET (rule 26)

99

GAATACTGAT	GAGTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGCCCCGT	GACTTTTCCT	300
CTCAGGCCTT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCCCTCA	GCCTCCACTC	AGGTCAGGAC	CAGAAGTCGC	TGTTCCCTTC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCGGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCGT	GCTGGTGGAG	TGTCCCATGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GTACCAGGGG	CCACGGGGCG	CCTTCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCAC	CCTCCCTCTG	GTCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CTCAATTAAG	GGATAAAATC	TCTGAAGGAG	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGCCCCGT	GACTTTTCCT	300
CTCAGGCCTT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCCCTCA	GCCTCCACTC	AGGTCAGGAC	CAGAAGTCGC	TGTTCCCTTC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCGGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCGT	GCTGGTGGAG	TGTCCCATGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GTACCAGGGG	CCACGGGGCG	CCTTCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCAC	CCTCCCTCTG	GTCTGAGGG	120

SUBSTITUTE SHEET (rule 26)

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AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAG	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGCCCCG	GACTTTTCCT	300
CTCAGGCCTT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCCCTCA	GCCTCCACTC	AGGTCAGGAC	CAGAAGTCGC	TGTTCCCTTC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCGGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCGT	GCTGGTGGAG	TGTCCCATGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTCTTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTGACCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

SUBSTITUTE SHEET (rule 26)

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GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0204

SUBSTITUTE SHEET (rule 26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 3 Allele A* 0205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no

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- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0206

(xi) SEQUENCE DESCRIPTION. SEQ ID NO:147:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CCTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCTTGACA    600
G

```

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CCTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCTTGACA    600
G

```

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCCT    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CCTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCTGACA    600
G                                                                    601

```

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCCT    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CCTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCTGACA    600
G                                                                    601

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(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CTTGTGTTCT TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCTTGACA    600
G                                                                    601

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(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CTTGTGTTCT TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC TTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGATCTGACT CTTCTTGACA    600
G                                                                    601

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(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTCAGCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 0217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTCAGCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480

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GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG 540
 TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGATCTGACT CTCCTGACA 600
 G 601

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 6801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA 60
 CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG 120
 AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGA CTCTGAG GTTCCGCCCT 180
 GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC 240
 GAATACTGAT GAGTGGTTCC CTTTGACACA CACAGGCAGC AGCCTTGGGC CCGTGACTTT 300
 TCCTCTCAGG CCTTGTTC TCCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC 360
 TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG 420
 ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG 480
 GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG 540
 TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGATCTGACT CTCCTGACA 600
 G 601

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 6802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA 60
 CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG 120
 AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGA CTCTGAG GTTCCGCCCT 180
 GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC 240

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GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 6901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACAGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	TTACGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGATCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

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GTACCAGGGG CCACGGGGCG CCTACCTGAT CGCCTGTAGG TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGA CTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGACGGAA TGACGGAAAG ACGATCCCTC    240
GAATACTGAT GACTGGTTCC CTTTGACACC GGCAGCAGCC TTGGGACCGT GACTTTTCCT    300
CTCAGGCCTT GTTCTCTGCT TCACACTCAA TGTGTGTGGG GGTCTGAGTC CAGCACTTCT    360
GAGTCCCTCA GCCTCCACTC AGGTCCAGGAC CAGAAGTCGC TGTTCCTCC TCAGGGAATA    420
GAAGATTATC CCAGGTGCCT GTGTCCAGGC TGGTGTCTGG GTTCTGTGCT CTCTTCCCCA    480
TCCCGGGTGT CCTGTCCATT CTCAAGATGG CCACATGCAT GCTGGTGGAG TGTCCCATGA    540
CAGATGCAAA ATGCCTGAAT TTTCTGACTC TTCCCGTCAG    580

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(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

GTACCAGGGG CCACGGGGCG CCTACCTGAT CGCCTGTAGG TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGA CTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGACGGAA TGACGGAAAG ACGATCCCTC    240
GAATACTGAT GACTGGTTCC CTTTGACACC GGCAGCAGCC TTGGGACCGT GACTTTTCCT    300
CTCAGGCCTT GTTCTCTGCT TCACACTCAA TGTGTGTGGG GGTCTGAGTC CAGCACTTCT    360
GAGTCCCTCA GCCTCCACTC AGGTCCAGGAC CAGAAGTCGC TGTTCCTCC TCAGGGAATA    420
GAAGATTATC CCAGGTGCCT GTGTCCAGGC TGGTGTCTGG GTTCTGTGCT CTCTTCCCCA    480
TCCCGGGTGT CCTGTCCATT CTCAAGATGG CCACATGCAT GCTGGTGGAG TGTCCCATGA    540
CAGATGCAAA ATGCCTGAAT TTTCTGACTC TTCCCGTCAG    580

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(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2403

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GTACCAGGGG	CCACGGGGCG	CCTACCTGAT	CGCCTGTAGG	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGACGGAA	TGACGGAAAG	ACGATCCCTC	240
GAATACTGAT	GACTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGACCGT	GACTTTTCCT	300
CTCAGGCCTT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCCCTCA	GCCTCCACTC	AGGTCAGGAC	CAGAAGTCGC	TGTTCCCTCC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCGGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCAT	GCTGGTGGAG	TGTCCCATGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GTACCAGGGG	CCACGGGGCG	CCTACCTGAT	CGCCTGTAGG	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGACGGAA	TGACGGAAAG	ACGATCCCTC	240
GAATACTGAT	GACTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGACCGT	GACTTTTCCT	300
CTCAGGCCTT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCCCTCA	GCCTCCACTC	AGGTCAGGAC	CAGAAGTCGC	TGTTCCCTCC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCGGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCAT	GCTGGTGGAG	TGTCCCATGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			579

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GTACCAGGGG	CCACGGGGCG	CCTACCTGAT	CGCCTGTAGG	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGACGGAA	TGACGGAAAG	ACGATCCCTC	240
GAATACTGAT	GACTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGACCGT	GACTTTTCCT	300
CTCAGGCCTT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCCCTCA	GCCTCCACTC	AGGTCAGGAC	CAGAAGTCGC	TGTTCCCTCC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCGGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCAT	GCTGGTGGAG	TGTCCCATGA	540
CAGATGCAAA	ATGCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 3 Allele A* 2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GTACCAGGGG	CCACGGGGCG	CCTACCTGAT	CGCCTGTAGG	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGACGGAA	TGACGGAAAG	ACGATCCCTC	240
GAATACTGAT	GACTGGTTCC	CTTTGACACC	GGCAGCAGCC	TTGGGACCGT	GACTTTTCCT	300
CTCAGGCCTT	GTTCTCTGCT	TCACACTCAA	TGTGTGTGGG	GGTCTGAGTC	CAGCACTTCT	360
GAGTCCCTCA	GCCTCCACTC	AGGTCAGGAC	CAGAAGTCGC	TGTTCCCTCC	TCAGGGAATA	420
GAAGATTATC	CCAGGTGCCT	GTGTCCAGGC	TGGTGTCTGG	GTTCTGTGCT	CTCTTCCCCA	480
TCCCGGGTGT	CCTGTCCATT	CTCAAGATGG	CCACATGCAT	GCTGGTGGAG	TGTCCCATGA	540
CAGATGCAAA	ATCCCTGAAT	TTTCTGACTC	TTCCCGTCAG			580

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 3 Allele A* 2501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGA CTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CCTTGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCTGACA    600
G                                                                    601

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(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 3 Allele A* 2601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGA CTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CCTTGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCTGACA    600
G                                                                    601

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(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no

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- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CCTTGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCTGACA    600
G                                                                    601

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(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 4301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CCTTGTTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCTGACA    600
G                                                                    601

```

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 3 Allele A* 6601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CTTGTCTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTCTGACT CTTCTGACA    600
G                                                                    601

```

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (ix) FEATURE:
 (A) NAME/KEY: HLA-A Intron 3 Allele A* 6602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA    60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG    120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT    180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC    240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT    300
TCCTCTCAGG CTTGTCTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC    360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG    420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG    480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG    540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTCTGACT CTTCTGACA    600
G                                                                    601

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(2) INFORMATION FOR SEQ ID NO:170:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 6603

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACCGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TTCTCTCAGG	CCTTGTTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGTTCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GTACCGGGG	CCACGGGGCG	CCTCCCTGAT	CGCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACCGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGTTCTGACT	CTTCCTGACA	600

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601

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 2902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GTACCGGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA 60
 CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG 120
 AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT 180
 GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC 240
 GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT 300
 TCCTCTCAGG CTTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC 360
 TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG 420
 ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG 480
 GGTCTGTGTC TCCTTCCCC ATCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG 540
 TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCTGACA 600
 G 601

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GTACCGGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA 60
 CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCCTGAGGG 120
 AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGACTCTGAG GTTCCGCCCT 180
 GCTCTGTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC 240
 GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT 300
 TCCTCTCAGG CTTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC 360

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TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG	120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGA CTCTGAG GTTCCGCCCT	180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC	240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT	300
TCCTCTCAGG CTTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC	360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG	420
ACTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG	480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG	540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTTCTGACT CTTCTGACA	600
G	601

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA	60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCAC CCTCCCTCTG GTCCTGAGGG	120

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AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTGTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACCGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCCT	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCAT	ACAGATGCAA	AATGCCTGAA	TGTTCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 3303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCAC	CCTCCCTCTG	GTCCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTGTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACCGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCCT	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCAT	ACAGATGCAA	AATGCCTGAA	TGTTCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: HLA-A Intron 3 Allele A* 7401

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACCGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGGG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCC	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGTTCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 3 Allele A*7402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GTACCAGGGG	CCACGGGGCG	CCTCCCTGAT	CGCCTGTAGA	TCTCCCGGGC	TGGCCTCCCA	60
CAAGGAGGGG	AGACAATTGG	GACCAACACT	AGAATATCGC	CCTCCCTCTG	GTCTGAGGG	120
AGAGGAATCC	TCCTGGGTTT	CCAGATCCTG	TACCAGAGAG	TGACTCTGAG	GTTCCGCCCT	180
GCTCTCTGAG	CACAATTAAG	GGATAAAATC	TCTGAAGGAA	TGACGGGAAG	ACGATCCCTC	240
GAATACTGAT	GAGTGGTTCC	CTTTGACACA	CACCGGCAGC	AGCCTTGGGC	CCGTGACTTT	300
TCCTCTCAGG	CCTTGTTCTC	TGCTTCACAC	TCAATGTGTG	TGGGGGTCTG	AGTCCAGCAC	360
TTCTGAGTCC	CTCAGCCTCC	ACTCAGGTCA	GGACCAGAAG	TCGCTGTTCC	CTCTTCAGCG	420
ACTAGAATTT	TCCACGGAAT	AGGAGATTAT	CCCAGGTGCT	TGTGTCCAGG	CTGGTGTCTG	480
GGTTCTGTGC	TCCCTTCCCC	ATCCCAGGTG	TCCTGTCCAT	TCTCAAGATA	GCCACATGTG	540
TGCTGGAGGA	GTGTCCCATG	ACAGATGCAA	AATGCCTGAA	TGTTCTGACT	CTTCCTGACA	600
G						601

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

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(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 3 Allele A* 7403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```

GTACCAGGGG CCACGGGGCG CCTCCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA 60
CAAGGAGGGG AGACAATTGG GACCAACACT AGAATATCGC CCTCCCTCTG GTCCTGAGGG 120
AGAGGAATCC TCCTGGGTTT CCAGATCCTG TACCAGAGAG TGA CTCTGAG GTTCCGCCCT 180
GCTCTCTGAG CACAATTAAG GGATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC 240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCAGC AGCCTTGGGC CCGTGACTTT 300
TCCTCTCAGG CCTTGTCTC TGCTTCACAC TCAATGTGTG TGGGGGTCTG AGTCCAGCAC 360
TTCTGAGTCC CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTCTTCAGGG 420
TCTAGAATTT TCCACGGAAT AGGAGATTAT CCCAGGTGCC TGTGTCCAGG CTGGTGTCTG 480
GGTTCTGTGC TCCCTTCCCC ATCCCAGGTG TCCTGTCCAT TCTCAAGATA GCCACATGTG 540
TGCTGGAGGA GTGTCCCATG ACAGATGCAA AATGCCTGAA TGTCTGACT CTTCTGACA 600
G 601

```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE:

(A) NAME/KEY: HLA-A Intron 3 Allele A* 8001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

GTACCAGGGG CCACGGGGCG CCTTCCTGAT CGCCTGTAGA TCTCCCGGGC TGGCCTCCCA 60
CAAGGAGGGG AGACAATTGG GACCAACACT AGATATCACC CTCCCTCTGC TCCTGAGGGA 120
GAGGAATCCT CCTGGGTTTC CAGATTCTGT ACCAGAGAGT GACTCTGAGG TTCCGCCCTG 180
CTCTCTGAGC ACAATTAAGG GATAAAATC TCTGAAGGAA TGACGGGAAG ACGATCCCTC 240
GAATACTGAT GAGTGGTTCC CTTTGACACA CACCGGCGGC AGCCTTGGGC CCGTGACTTT 300
TCCTCTCAGG CCCTGTCTC TGCTTCACAC TCAATATGTG TGGGGGTCTG AGTCCAGCAC 360
TTCTGAGTCT CTCAGCCTCC ACTCAGGTCA GGACCAGAAG TCGCTGTTCC CTGCTCAGGG 420
AATAGAAGAT TATCCAGGT GCCTGTGTCC AGGCTGGTGT CTGGGTTCTG TGCTCTCTTC 480
CCCATCCCAG GTGTCCTGTC CATCCTCAA ATGGCCACAT GCGTGCTGGT GGAGTGTCCC 540
ATGACAGATG CAAATGGCT GAATTTTCTG ACTCTTCCCG TCAG 584

```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no

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- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: Il-230m

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GGCAGGTCTC AGCGACTG

18

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Il-226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CTCTGTGGGG AGAAGCAAC

19

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Il-221ml1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GGGAGCGGCG CCGGGAC

17

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Il-209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAAGCAAGGG GCCCCCCC

18

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Il-214m

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

CGCCTGGCGG GGGGGCAA

18

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Il-223d

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GTGAGTGCGG GGTCGTGG

18

(2) INFORMATION FOR SEQ ID NO:187:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Il-225m

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GCCGGGAGGA GGGACGGT

18

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Il-237m14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GGCGCGCCCG GCGGGGA

17

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Il-240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

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GGAGGAGGGT CGGGCGGA

18

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 5FL-243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

AGTGTCTTCG CGGTCGCTC

19

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 5FR-257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTCAGATTCT CCCCAGACG

19

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 5FR-273

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CATGCCGAGG GTTTCTCCCA

20

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: BP202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

CTGGCCCTGA CCCAGACCA

19

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: BP203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

CCTGACCCAG ACCTGGGCA

19

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:

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- (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: BP142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CAGGTATCTG CGGAGCCCG

19

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: I3-236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GTCTGTCAGG AAGAGTCAGA A

21

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: I3-239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GTGGAAAATT CTAGTCCCTG AA

22

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: I3-246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

AGATCTACAG GCGATCAGGA

20

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: I3-247m6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCCAGCCCCG GAGTTCTAT

19

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: I3-249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CAGAGTCACT CTCTGGTACA G

21

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: I3-280m18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GCGATCGTCT TCCCGTCAC

19

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: I3-282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

AGAGTCACTC TCTGGTACAG A

21

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CTCCTCGTCC CCAGGCTCT

19

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(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TCCATGAGGT ATTTCTACAC C

21

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGCCAGGTTC TCAGACCA

18

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 123

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCCGGCCCGG CAGTGA

17

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GTTCTCACAC CATCCAGATG

20

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TCACACCCTC CAGATGATGT T

21

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

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- (ix) FEATURE:
(A) NAME/KEY: 134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTACCAGC AGGACGCT

18

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: 137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

TCCATGAGGT ATTCACCAC A

21

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE:
(A) NAME/KEY: 140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GGTTCTCACA CCATCCAGAT A

21

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA

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- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: 160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GTTCTCACAC CATCCAGAGG

20

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: 167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GAGCCCCGCT TCAACGCC

18

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: 175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CTTCCTCCGC GGGTATGAA

19

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GCCGGAGTAT TGGGACCG

18

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGGCCCTGA CCCTGACCA

19

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GCAGGGTCCC CAGGTCCA

18

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(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CCTCCAGGTA GGCTCTCAA

19

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

CCTCCAGGTA GGCTCTCCA

19

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 117

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

CCTCCAGGTA GGCTCTCTG

19

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CCTCTCCAGC CACGTGCCA

19

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GGAGCGCGAT CCGCAGGC

18

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

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- (ix) FEATURE:
 - (A) NAME/KEY: 135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GGAGCCACTC CACGGACCG

19

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GAGCCACTCC ACGCACTC

18

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGCCTTCACA TTCCGTGTGT T

21

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

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- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: 142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

CAGGTATCTG CGGAGCCCG

19

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

TGGTCCCAAT ACTCAGGCCT

20

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GCAGGGTCCC CAGGTTCG

18

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GGGCCGCCTC CCA GTTGT

18

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TCTGTGAGTG GGCCTACACA

20

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CCTTCACATT CCGTGTCTGC A

21

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(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GAGCCACTCC ACGCACGT

18

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CCACTCGGTC AGTCTCTGAC

20

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 165

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAGCGCAGGT CCTCGTTCAA

20

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GTCTGTGAGT GGGCCATCAT

20

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

CAGCCATACA TCCTCAGGAC

20

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human

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- (ix) FEATURE:
(A) NAME/KEY: Ex2 (Aw3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GCGCCGGGAG GAGGGTC

17

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
- (ix) FEATURE:
(A) NAME/KEY: Ex2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

ATCTCGGACC CGGAGACT

18

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(v) ORIGINAL SOURCE:
(A) ORGANISM: human
- (ix) FEATURE:
(A) NAME/KEY: Ex3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GTTTCATTTT CAGTTTAGGC CA

22

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA

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- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
- (ix) FEATURE:
 - (A) NAME/KEY: Ex3 (Aw6)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

CGGGAGATCT ACAGGCGATC AGG

23

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Ex2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GTCGTGACCT GCGCCCC

17

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Ex3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GGGCGGGGCG GGGCTCGGG

19

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Ex2 (ABCw1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GGTCGTGACC TTCCGCCCC

19

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: Ex3 (ABCw2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CCCGGTTTCA TTTTC

15

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (ix) FEATURE:
 - (A) NAME/KEY: 119

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

CTTACATTTC CGTGTCTCCT

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WHAT IS CLAIMED IS:

1. A method of determining the HLA Class I group type of a subject comprising the following steps:

(i) combining a group-specific untranslated region primer pair with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur; and

(ii) determining whether a nucleic acid product is produced by the amplification;

wherein the ability of the primer pair to produce a nucleic acid product is associated with a particular HLA group type.

2. The method of claim 1, wherein the HLA Class I group to be determined is part of the HLA-A locus.

3. The method of claim 1, further comprising the step of (iii) determining the nucleic acid sequence of the nucleic acid product of step (ii).

4. The method of claim 1, wherein the primer pair comprises one or more oligonucleotide primers selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO:184), I1-214m (SEQ ID NO:185), I1-223d (SEQ ID NO:186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202).

5. The method of claim 1, wherein the primer pair is selected from the group of pairs consisting of I1-230m (SEQ ID NO:181) and BP142 (SEQ ID NO:195); 5'FR-257 (SEQ ID NO:191) and I3-247m6 (SEQ ID NO:199); I1-230m (SEQ ID NO:181) and I3-247m6 (SEQ ID NO:199); I1-226 (SEQ ID NO:182) and I3-249 (SEQ ID NO:200); I1-221m11 (SEQ ID NO:183) and I3-280m18 (SEQ ID

NO:201); 5'FL-243 (SEQ ID NO:190) and I3-249 (SEQ ID NO:200); I1-214m (SEQ ID NO:185) and I3-249 (SEQ ID NO:200); I1-210m (SEQ ID NO:35) and I3-236 (SEQ ID NO:196); I1-210m (SEQ ID NO:35) and I3-249 (SEQ ID NO:200); 5'FR-273 (SEQ ID NO:192) and I3-249 (SEQ ID NO:200); I1-223d (SEQ ID NO:186) and I3-239 (SEQ ID NO:197); I1-223d (SEQ ID NO:186) and I3-249 (SEQ ID NO:200); I1-240 (SEQ ID NO:189) and I3-249 (SEQ ID NO:200); I1-237m14 (SEQ ID NO:188) and I3-249 (SEQ ID NO:200); I1-225m (SEQ ID NO:187) and I3-249 (SEQ ID NO:200); BP202 (SEQ ID NO:193) and I3-249 (SEQ ID NO:200) and BP203 (SEQ ID NO:194) and I3-282 (SEQ ID NO:202).

6. A method of determining the HLA Class I allele type of a subject comprising the following steps:

(i) combining a group-specific exon region primer pair with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur;

(ii) determining whether a first nucleic acid product is produced by the amplification wherein the ability of the primer pair to produce a nucleic acid product is associated with a particular HLA group type, and thereby identifying the group type;

(iii) combining a group-specific untranslated region primer pair corresponding to the group type of the subject, as determined by steps (i)-(ii), with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur and a second nucleic acid product is produced; and

(iv) determining the nucleic acid sequence of the second nucleic acid product collected in step (iii).

7. The method of claim 6, wherein the HLA Class I allele to be determined is part of the HLA-A locus.

8. The method of claim 6, wherein the group-specific exon region primer pair used in step (i) comprises one or more oligonucleotide primers selected

from the group consisting of primers 85 (SEQ ID NO:203), 118 (SEQ ID NO:204), 120 (SEQ ID NO:205), 123 (SEQ ID NO:206), 127 (SEQ ID NO:207), 129 (SEQ ID NO:208), 134 (SEQ ID NO:209), 137 (SEQ ID NO:210), 140 (SEQ ID NO:211), 160 (SEQ ID NO:212), 167 (SEQ ID NO:213), 175 (SEQ ID NO:214), 193 (SEQ ID NO:215), 202 (SEQ ID NO:216), 98 (SEQ ID NO:217), 115 (SEQ ID NO:218), 116 (SEQ ID NO:219), 117 (SEQ ID NO:220), 119 (SEQ ID NO:245), 126 (SEQ ID NO:221), 133 (SEQ ID NO:222), 135 (SEQ ID NO:223), 136 (SEQ ID NO:224), 138 (SEQ ID NO:225), 142 (SEQ ID NO:226), 144 (SEQ ID NO:227), 145 (SEQ ID NO:228), 152 (SEQ ID NO:229), 153 (SEQ ID NO:230), 154 (SEQ ID NO:231), 155 (SEQ ID NO:232), 161 (SEQ ID NO:233), 165 (SEQ ID NO:234), 168 (SEQ ID NO:235) and 180 (SEQ ID NO:236).

9. The method of claim 6, wherein the group-specific exon region primer pair used in step (i) is selected from the group of pairs consisting of 140 (SEQ ID NO:211) and 142 (SEQ ID NO:226); 85 (SEQ ID NO:203) and 98 (SEQ ID NO:217); 140 (SEQ ID NO:211) and 126 (SEQ ID NO:221); 167 (SEQ ID NO:213) and 168 (SEQ ID NO:235); 118 (SEQ ID NO:204) and 119 (SEQ ID NO:245); 129 (SEQ ID NO:208) and 115 (SEQ ID NO:218); 129 (SEQ ID NO:208) and 116 (SEQ ID NO:219) and 117 (SEQ ID NO:220); 160 (SEQ ID NO:212) and 135 (SEQ ID NO:223); 118 (SEQ ID NO:204) and 133 (SEQ ID NO:222); 118 (SEQ ID NO:204) and 145 (SEQ ID NO:228); 134 (SEQ ID NO:209) and 155 (SEQ ID NO:232); 134 (SEQ ID NO:209) and 136 (SEQ ID NO:224); 118 (SEQ ID NO:204) and 161 (SEQ ID NO:233); 118 (SEQ ID NO:204) and 154 (SEQ ID NO:231); 120 (SEQ ID NO:205) and 152 (SEQ ID NO:229); 193 (SEQ ID NO:215) and 180 (SEQ ID NO:236); 127 (SEQ ID NO:207) and 165 (SEQ ID NO:234); 137 (SEQ ID NO:210) and 145 (SEQ ID NO:228); 175 (SEQ ID NO:214) and 115 (SEQ ID NO:218) and 116 (SEQ ID NO:219); 167 (SEQ ID NO:213) and 144 (SEQ ID NO:227); 167 (SEQ ID NO:213) and 133 (SEQ ID NO:222); 137 (SEQ ID NO:210) and 138 (SEQ ID NO:225); 202 (SEQ ID NO:216) and 153 (SEQ ID NO:230); and 140 (SEQ ID NO:211) and 136 (SEQ ID NO:224).

10. The method of claim 6, wherein the group-specific untranslated region primer pair used in step (iii) comprises one or more oligonucleotide primers selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO:184), I1-214m (SEQ ID NO:185), I1-223d (SEQ ID NO:186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202).

11. The method of claim 6, wherein the group-specific untranslated region primer pair used in step (iii) is selected from the group of oligonucleotide primer pairs consisting of I1-230m (SEQ ID NO:181) and BP142 (SEQ ID NO:195); 5'FR-257 (SEQ ID NO:191) and I3-247m6 (SEQ ID NO:199); I1-230m (SEQ ID NO:181) and I3-247m6 (SEQ ID NO:199); I1-226 (SEQ ID NO:182) and I3-249 (SEQ ID NO:200); I1-221m11 (SEQ ID NO:183) and I3-280m18 (SEQ ID NO:201); 5'FL-243 (SEQ ID NO:190) and I3-249 (SEQ ID NO:200); I1-214m (SEQ ID NO:185) and I3-249 (SEQ ID NO:200); I1-210m (SEQ ID NO:35) and I3-236 (SEQ ID NO:196); I1-210m (SEQ ID NO:35) and I3-249 (SEQ ID NO:200); 5'FR-273 (SEQ ID NO:192) and I3-249 (SEQ ID NO:200); I1-223d (SEQ ID NO:186) and I3-239 (SEQ ID NO:197); I1-223d (SEQ ID NO:186) and I3-249 (SEQ ID NO:200); I1-240 (SEQ ID NO:189) and I3-249 (SEQ ID NO:200); I1-237m14 (SEQ ID NO:188) and I3-249 (SEQ ID NO:200); I1-225m (SEQ ID NO:187) and I3-249 (SEQ ID NO:200); BP202 (SEQ ID NO:193) and I3-249 (SEQ ID NO:200) and BP203 (SEQ ID NO:194) and I3-282 (SEQ ID NO:202).

12. A method of determining the HLA Class I allele type of a subject comprising the following steps:

(i) combining a plurality of group-specific exon region primer pairs

with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur and a first nucleic acid product is produced;

(ii) determining the size of the first nucleic acid product of the amplification;

(iii) correlating the size of the first nucleic acid product with the predicted size of a fragment associated with a particular HLA type;

(iv) combining a group-specific untranslated region primer pair corresponding to the group type of the subject, as determined by steps (i)-(iii), with a target DNA sample from the subject under conditions such that primer-based amplification of the target DNA may occur and a second nucleic acid product is produced; and

(v) determining the nucleic acid sequence of the second nucleic acid product.

13. The method of claim 12, wherein the HLA Class I allele to be determined is part of the HLA-A locus.

14. The method of claim 12, wherein the plurality of group-specific exon region primer pairs used in step (i) comprises one or more oligonucleotide primers selected from the group consisting of primers 85 (SEQ ID NO:203), 118 (SEQ ID NO:204), 120 (SEQ ID NO:205), 123 (SEQ ID NO:206), 127 (SEQ ID NO:207), 129 (SEQ ID NO:208), 134 (SEQ ID NO:209), 137 (SEQ ID NO:210), 140 (SEQ ID NO:211), 160 (SEQ ID NO:212), 167 (SEQ ID NO:213), 175 (SEQ ID NO:214), 193 (SEQ ID NO:215), 202 (SEQ ID NO:216), 98 (SEQ ID NO:217), 115 (SEQ ID NO:218), 116 (SEQ ID NO:219), 117 (SEQ ID NO:220), 126 (SEQ ID NO:221), 133 (SEQ ID NO:222), 135 (SEQ ID NO:223), 136 (SEQ ID NO:224), 138 (SEQ ID NO:225), 142 (SEQ ID NO:226), 144 (SEQ ID NO:227), 145 (SEQ ID NO:228), 152 (SEQ ID NO:229), 153 (SEQ ID NO:230), 154 (SEQ ID NO:231), 155 (SEQ ID NO:232), 161 (SEQ ID NO:233), 165 (SEQ ID NO:234), 168 (SEQ ID NO:235) and 180 (SEQ ID NO:236).

15. The method of claim 12, wherein the plurality of group-specific exon region primer pairs used in step (i) comprises one or more oligonucleotide primer pairs selected from the group of pairs consisting of 140 (SEQ ID NO:211) and 142 (SEQ ID NO:226); 85 (SEQ ID NO:203) and 98 (SEQ ID NO:217); 140 (SEQ ID NO:211) and 126 (SEQ ID NO:221); 167 (SEQ ID NO:213) and 168 (SEQ ID NO:235); 118 (SEQ ID NO:204) and 119 (SEQ ID NO:245); 129 (SEQ ID NO:208) and 115 (SEQ ID NO:218); 129 (SEQ ID NO:208) and 116 (SEQ ID NO:219) and 117 (SEQ ID NO:220); 160 (SEQ ID NO:212) and 135 (SEQ ID NO:223); 118 (SEQ ID NO:204) and 133 (SEQ ID NO:222); 118 (SEQ ID NO:204) and 145 (SEQ ID NO:228); 134 (SEQ ID NO:209) and 155 (SEQ ID NO:232); 134 (SEQ ID NO:209) and 136 (SEQ ID NO:224); 118 (SEQ ID NO:204) and 161 (SEQ ID NO:233); 118 (SEQ ID NO:204) and 154 (SEQ ID NO:231); 120 (SEQ ID NO:205) and 152 (SEQ ID NO:229); 193 (SEQ ID NO:215) and 180 (SEQ ID NO:236); 127 (SEQ ID NO:207) and 165 (SEQ ID NO:234); 137 (SEQ ID NO:210) and 145 (SEQ ID NO:228); 175 (SEQ ID NO:214) and 115 (SEQ ID NO:218) and 116 (SEQ ID NO:219); 167 (SEQ ID NO:213) and 144 (SEQ ID NO:227); 167 (SEQ ID NO:213) and 133 (SEQ ID NO:222); 137 (SEQ ID NO:210) and 138 (SEQ ID NO:225); 202 (SEQ ID NO:216) and 153 (SEQ ID NO:230); and 140 (SEQ ID NO:211) and 136 (SEQ ID NO:224).

16. The method of claim 12, wherein the group-specific untranslated region primer pair used in step (iv) comprises one or more oligonucleotide primers selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO:184), I1-214m (SEQ ID NO:185), I1-223d (SEQ ID NO:186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ

ID NO:202).

17. The method of claim 12, wherein the group-specific untranslated region primer pair used in step (iv) is selected from the group of oligonucleotide primer pairs consisting of I1-230m (SEQ ID NO:181) and BP142 (SEQ ID NO:195); 5'FR-257 (SEQ ID NO:191) and I3-247m6 (SEQ ID NO:199); I1-230m (SEQ ID NO:181) and I3-247m6 (SEQ ID NO:199); I1-226 (SEQ ID NO:182) and I3-249 (SEQ ID NO:200); I1-221m11 (SEQ ID NO:183) and I3-280m18 (SEQ ID NO:201); 5'FL-243 (SEQ ID NO:190) and I3-249 (SEQ ID NO:200); I1-214m (SEQ ID NO:185) and I3-249 (SEQ ID NO:200); I1-210m (SEQ ID NO:35) and I3-236 (SEQ ID NO:196); I1-210m (SEQ ID NO:35) and I3-249 (SEQ ID NO:200); 5'FR-273 (SEQ ID NO:192) and I3-249 (SEQ ID NO:200); I1-223d (SEQ ID NO:186) and I3-239 (SEQ ID NO:197); I1-223d (SEQ ID NO:186) and I3-249 (SEQ ID NO:200); I1-240 (SEQ ID NO:189) and I3-249 (SEQ ID NO:200); I1-237m14 (SEQ ID NO:188) and I3-249 (SEQ ID NO:200); I1-225m (SEQ ID NO:187) and I3-249 (SEQ ID NO:200); BP202 (SEQ ID NO:193) and I3-249 (SEQ ID NO:200) and BP203 (SEQ ID NO:194) and I3-282 (SEQ ID NO:202).

18. A composition comprising a plurality of oligonucleotide primer pairs comprising one or more primers selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO:184), I1-214m (SEQ ID NO:185), I1-223d (SEQ ID NO:186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202).

19. A composition comprising an oligonucleotide primer selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO:184), I1-

214m (SEQ ID NO: 185), I1-223d (SEQ ID NO: 186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202).

20. A composition comprising an oligonucleotide primer pair selected from the group consisting of I1-230m (SEQ ID NO:181) and BP142 (SEQ ID NO:195); 5'FR-257 (SEQ ID NO:191) and I3-247m6 (SEQ ID NO:199); I1-230m (SEQ ID NO:181) and I3-247m6 (SEQ ID NO:199); I1-226 (SEQ ID NO:182) and I3-249 (SEQ ID NO:200); I1-221m11 (SEQ ID NO:183) and I3-280m18 (SEQ ID NO:201); 5'FL-243 (SEQ ID NO:190) and I3-249 (SEQ ID NO:200); I1-214m (SEQ ID NO:185) and I3-249 (SEQ ID NO:200); I1-210m (SEQ ID NO:35) and I3-236 (SEQ ID NO:196); I1-210m (SEQ ID NO:35) and I3-249 (SEQ ID NO:200); 5'FR-273 (SEQ ID NO:192) and I3-249 (SEQ ID NO:200); I1-223d (SEQ ID NO:186) and I3-239 (SEQ ID NO:197); I1-223d (SEQ ID NO:186) and I3-249 (SEQ ID NO:200); I1-240 (SEQ ID NO:189) and I3-249 (SEQ ID NO:200); I1-237m14 (SEQ ID NO:188) and I3-249 (SEQ ID NO:200); I1-225m (SEQ ID NO:187) and I3-249 (SEQ ID NO:200); BP202 (SEQ ID NO:193) and I3-249 (SEQ ID NO:200) and BP203 (SEQ ID NO:194) and I3-282 (SEQ ID NO:202).

21. A kit comprising:

(a) a plurality of oligonucleotide group-specific untranslated region primer pairs comprising one or more primers selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO: 184), I1-214m (SEQ ID NO: 185), I1-223d (SEQ ID NO: 186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID

NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202); and

(b) an enzyme for nucleotide chain extension.

22. A kit comprising:

(a) an oligonucleotide group-specific untranslated region primer selected from the group consisting of I1-210m (SEQ ID NO:35), I1-230m (SEQ ID NO:181), I1-226 (SEQ ID NO:182), I1-221m11 (SEQ ID NO:183), I1-209 (SEQ ID NO:184), I1-214m (SEQ ID NO:185), I1-223d (SEQ ID NO:186), I1-225m (SEQ ID NO:187), I1-237m14 (SEQ ID NO:188), I1-240 (SEQ ID NO:189), 5'FL-243 (SEQ ID NO:190), 5'FR-257 (SEQ ID NO:191), 5'FR-273 (SEQ ID NO:192), BP202 (SEQ ID NO:193), BP203 (SEQ ID NO:194), BP142 (SEQ ID NO:195), I3-236 (SEQ ID NO:196), I3-239 (SEQ ID NO:197), I3-246 (SEQ ID NO:198), I3-247m6 (SEQ ID NO:199), I3-249 (SEQ ID NO:200), I3-280m18 (SEQ ID NO:201) and I3-282 (SEQ ID NO:202); and

(b) an enzyme for nucleotide chain extension.

23. The kit of claim 22, further comprising:

(c) a cocktail comprising group-specific exon region primers comprising one or more primer selected from the group consisting of 85 (SEQ ID NO:203), 118 (SEQ ID NO:204), 120 (SEQ ID NO:205), 123 (SEQ ID NO:206), 127 (SEQ ID NO:207), 129 (SEQ ID NO:208), 134 (SEQ ID NO:209), 137 (SEQ ID NO:210), 140 (SEQ ID NO:211), 160 (SEQ ID NO:212), 167 (SEQ ID NO:213), 175 (SEQ ID NO:214), 193 (SEQ ID NO:215), 202 (SEQ ID NO:216), 98 (SEQ ID NO:217), 115 (SEQ ID NO:218), 116 (SEQ ID NO:219), 117 (SEQ ID NO:220), 126 (SEQ ID NO:221), 133 (SEQ ID NO:222), 135 (SEQ ID NO:223), 136 (SEQ ID NO:224), 138 (SEQ ID NO:225), 142 (SEQ ID NO:226), 144 (SEQ ID NO:227), 145 (SEQ ID NO:228), 152 (SEQ ID NO:229), 153 (SEQ ID NO:230), 154 (SEQ ID NO:231), 155 (SEQ ID NO:232), 161 (SEQ ID NO:233), 165 (SEQ ID NO:234), 168 (SEQ ID NO:235) and 180 (SEQ ID NO:236).

24. A kit comprising:

(a) an oligonucleotide primer pair selected from the group consisting of

I1-230m (SEQ ID NO:181) and BP142 (SEQ ID NO:195); 5'FR-257 (SEQ ID NO:191) and I3-247m6 (SEQ ID NO:199); I1-230m (SEQ ID NO:181) and I3-247m6 (SEQ ID NO:199); I1-226 (SEQ ID NO:182) and I3-249 (SEQ ID NO:200); I1-221m11 (SEQ ID NO:183) and I3-280m18 (SEQ ID NO:201); 5'FL-243 (SEQ ID NO:190) and I3-249 (SEQ ID NO:200); I1-214m (SEQ ID NO:185) and I3-249 (SEQ ID NO:200); I1-210m (SEQ ID NO:35) and I3-236 (SEQ ID NO:196); I1-210m (SEQ ID NO:35) and I3-249 (SEQ ID NO:200); 5'FR-273 (SEQ ID NO:192) and I3-249 (SEQ ID NO:200); I1-223d (SEQ ID NO:186) and I3-239 (SEQ ID NO:197); I1-223d (SEQ ID NO:186) and I3-249 (SEQ ID NO:200); I1-240 (SEQ ID NO:189) and I3-249 (SEQ ID NO:200); I1-237m14 (SEQ ID NO:188) and I3-249 (SEQ ID NO:200); I1-225m (SEQ ID NO:187) and I3-249 (SEQ ID NO:200); BP202 (SEQ ID NO:193) and I3-249 (SEQ ID NO:200) and BP203 (SEQ ID NO:194) and I3-282 (SEQ ID NO:202); and

(b) an enzyme for nucleotide chain extension..

25. The kit of claim 24, further comprising:

(c) a cocktail comprising group-specific exon region primers

comprising one or more primer selected from the group consisting of 85 (SEQ ID NO:203), 118 (SEQ ID NO:204), 120 (SEQ ID NO:205), 123 (SEQ ID NO:206), 127 (SEQ ID NO:207), 129 (SEQ ID NO:208), 134 (SEQ ID NO:209), 137 (SEQ ID NO:210), 140 (SEQ ID NO:211), 160 (SEQ ID NO:212), 167 (SEQ ID NO:213), 175 (SEQ ID NO:214), 193 (SEQ ID NO:215), 202 (SEQ ID NO:216), 98 (SEQ ID NO:217), 115 (SEQ ID NO:218), 116 (SEQ ID NO:219), 117 (SEQ ID NO:220), 126 (SEQ ID NO:221), 133 (SEQ ID NO:222), 135 (SEQ ID NO:223), 136 (SEQ ID NO:224), 138 (SEQ ID NO:225), 142 (SEQ ID NO:226), 144 (SEQ ID NO:227), 145 (SEQ ID NO:228), 152 (SEQ ID NO:229), 153 (SEQ ID NO:230), 154 (SEQ ID NO:231), 155 (SEQ ID NO:232), 161 (SEQ ID NO:233), 165 (SEQ ID NO:234), 168

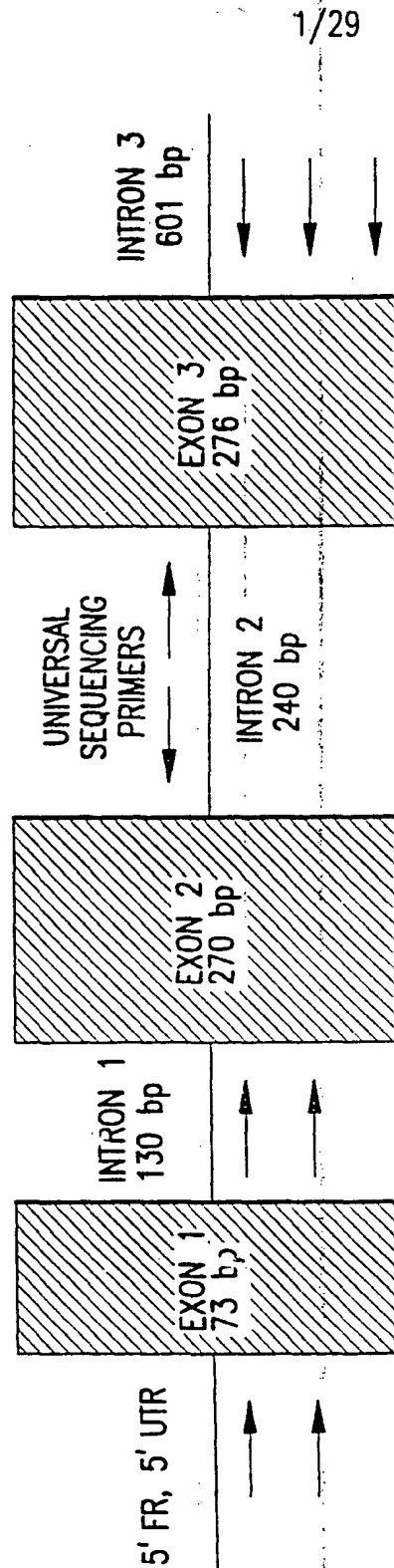
(SEQ ID NO:235) and 180 (SEQ ID NO:236).

(b) an enzyme for nucleotide chain extension..

26. The kit of claim 25, further comprising:

(d) a sequencing primer selected from the group consisting of 5'-

EX2(Aw3) 5' GCG GCG GGA GGA GGG TC 3' (SEQ ID NO:237), 3'-Ex2 5' ATC
TCG GAC CCG GAG ACT 3' (SEQ ID NO:238), 5' GTT TCA TTT TCA GTT TAG
GCC A 3' (SEQ ID NO:239), 3'-Ex3 (Aw6) 5' CGG GAG ATC TAC AGG CGA
TCA GG 3' (SEQ ID NO:241), 5'-Ex3 5'GGG CGG GGC GGG GCT CGG G3
(SEQ ID NO:242), 3'-Ex2 (ABCw1) 5' GGT CGT GAC CT(T/C)CGC CCC 3' (SEQ
ID NO:243), and 5'-Ex3 (ABCw2) 5' CCC GGT TTC ATT TTC 3' (SEQ ID
NO:244).



GROUP-SPECIFIC NON-CODING REGION PRIMERS

FIG.1

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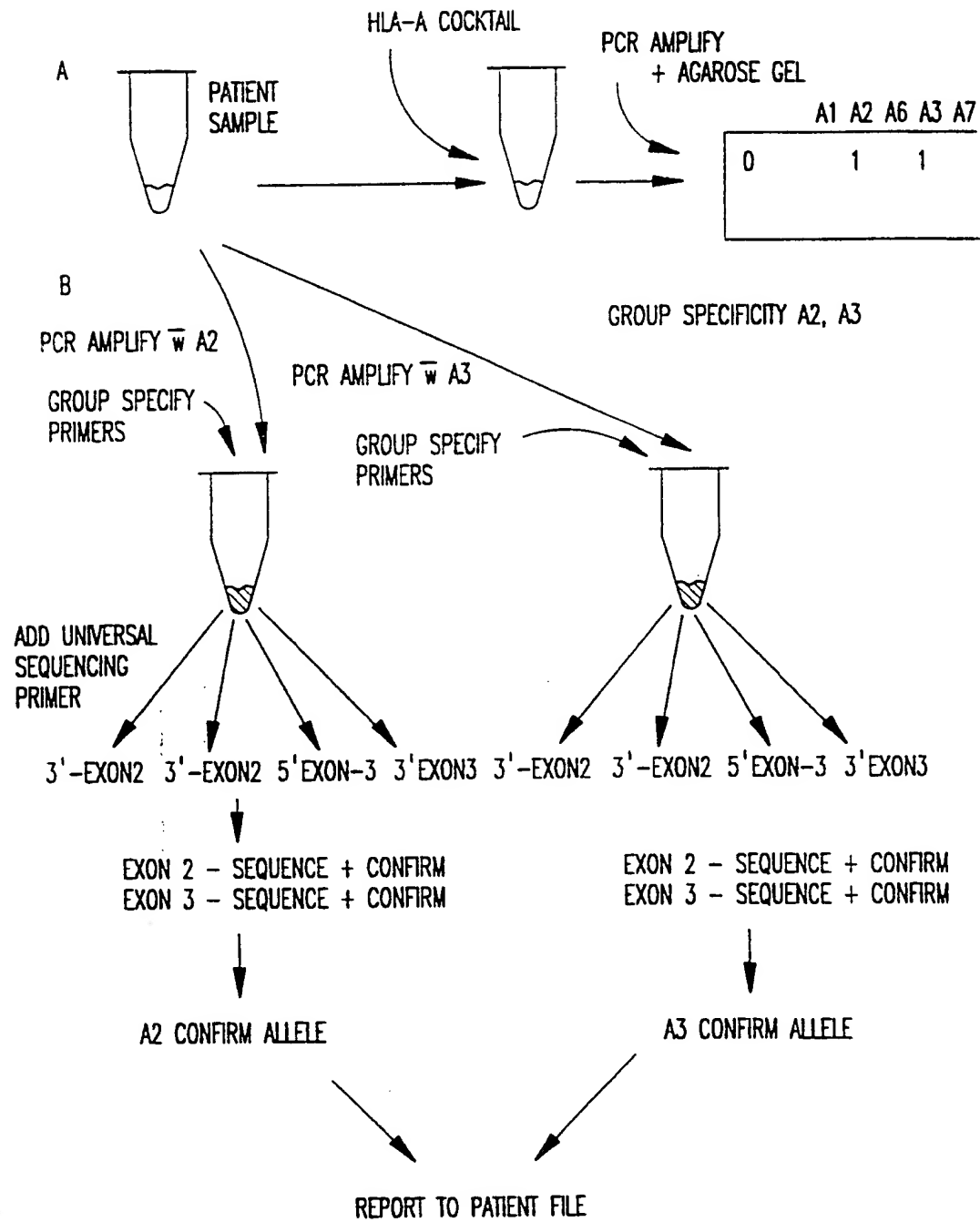


FIG.2(1)

SUBSTITUTE SHEET (rule 26)

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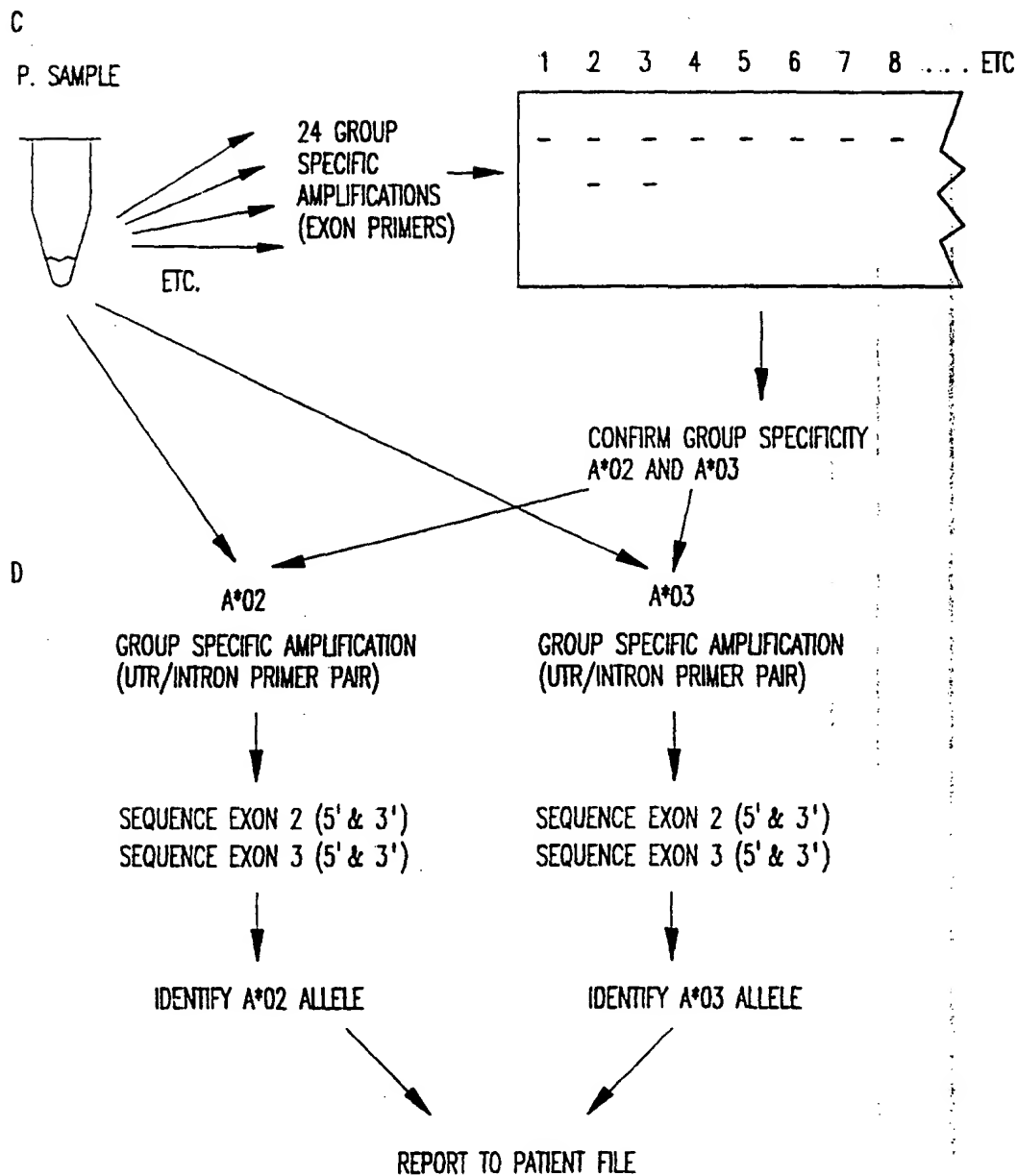


FIG.2(2)

HLA-A 5' flankierende Region. Teil I

[illegible]

FIG. 3A

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HLA-A 5'flankierende Region. Teil II

	110	120	130	140	150	160	170	180	190	200
Gonsensus	CTCTTGACCCAGGCGAGCACTAGGTCCTTCTTCCTGGGATGTATCCAAACCTCTCCCTCTTTTCTTTGACGCCCTCAACCCCTTAGGGGTTCGGACC									
A*0101	-----	-----	-----	A-----	-----	-----	-----	-----	-----	-----
A*0301	-----	-----	-----	A-----	-----	-----	-----	-----	-----	-----
A*1101	-----	-----	-----	A-----	-----	-----	-----	-----	-----	-----
A*1102	-----	-----	-----	A-----	-----	-----	-----	-----	-----	-----
A*3001	-----	-----	-----	A-----	-----	-----	-----	-----	-----	A-----
A*3002	-----	-----	-----	A-----	-----	-----	-----	-----	-----	A-----
A*3004	-----	-----	-----	A-----	-----	-----	-----	-----	-----	A-----
A*0201-11	-----	-----	-----	A-----	-----	-----	-----	-----	-----	-----
A*0215	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*0217	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*6801	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*6802	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*6901	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2301	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2402	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2403	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2404	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2405	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2407	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2501	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2601	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*3402	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*4301	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*6601	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*6602	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*6603	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2901	-----	-----	-----	-----	-----	G-----	-----	-----	-----	-----
A*2902	-----	-----	-----	-----	-----	G-----	-----	-----	-----	-----
A*31012	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*3201	-----	-----	-----	-----	-----	G-----	-----	-----	-----	-----
A*3301	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*3303	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*7401	-----	-----	-----	-----	-----	G-----	-----	-----	-----	-----
A*7402	-----	-----	-----	-----	-----	G-----	-----	-----	-----	-----
A*7403	-----	-----	-----	-----	-----	G-----	-----	-----	-----	-----
A*8001	-----	-----	-----	-----	-----	-----	-----	-----	-----	A-----

FIG.3B

SUBSTITUTE SHEET (RULE 26)

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HLA-A 5'flankierende Region. Teil III

	210	220	230	240	250	260	270	280	290	300
Consensus	CTGAGGGGTTAGGTA	TGTTGGGGAAGCC	CGGACCTCTGGGAC	CTCTGGGACCTCT	GGGACCTCTGGGAC	CTCTGGGACCTCT	GGGACCTCTGGGAC	CTCTGGGACCTCT	GGGACCTCTGGGAC	CTCTGGGACCTCT
A*0101	---	---	---	---	---	---	---	---	---	---
A*0301	---	---	---	---	---	---	---	---	---	---
A*1101	---	---	---	---	---	---	---	---	---	---
A*1102	---	---	---	---	---	---	---	---	---	---
A*3001	---	---	---	---	---	---	---	---	---	---
A*3002	---	---	---	---	---	---	---	---	---	---
A*3004	---	---	---	---	---	---	---	---	---	---
A*0201-11	---	---	---	---	---	---	---	---	---	---
A*0215	---	---	---	---	---	---	---	---	---	---
A*0217	---	---	---	---	---	---	---	---	---	---
A*6801	---	---	---	---	---	---	---	---	---	---
A*6802	---	---	---	---	---	---	---	---	---	---
A*6901	---	---	---	---	---	---	---	---	---	---
A*2301	---	---	---	---	---	---	---	---	---	---
A*2402	---	---	---	---	---	---	---	---	---	---
A*2403	---	---	---	---	---	---	---	---	---	---
A*2404	---	---	---	---	---	---	---	---	---	---
A*2405	---	---	---	---	---	---	---	---	---	---
A*2407	---	---	---	---	---	---	---	---	---	---
A*2501	---	---	---	---	---	---	---	---	---	---
A*2601	---	---	---	---	---	---	---	---	---	---
A*3402	---	---	---	---	---	---	---	---	---	---
A*4301	---	---	---	---	---	---	---	---	---	---
A*6601	---	---	---	---	---	---	---	---	---	---
A*6602	---	---	---	---	---	---	---	---	---	---
A*6603	---	---	---	---	---	---	---	---	---	---
A*2901	---	---	---	---	---	---	---	---	---	---
A*2902	---	---	---	---	---	---	---	---	---	---
A*31012	---	---	---	---	---	---	---	---	---	---
A*3201	---	---	---	---	---	---	---	---	---	---
A*3301	---	---	---	---	---	---	---	---	---	---
A*3303	---	---	---	---	---	---	---	---	---	---
A*7401	---	---	---	---	---	---	---	---	---	---
A*7402	---	---	---	---	---	---	---	---	---	---
A*7403	---	---	---	---	---	---	---	---	---	---
A*8001	---	---	---	---	---	---	---	---	---	---

FIG.3C

SUBSTITUTE SHEET (RULE 26)

7/29

HLA-A 5' flanking Region, Teil IV

Consensus	310	320	330	340	350	360	370	380	390	400
A*0101	GAGACAGAGTTACAGAGGGACTCAGAACCGGTTCTCGACAGACTCTTTGTTCCCTCTTTTGGGAGCCGTACCCGGGGCAGGGAGAGGAAAGTGAAAAAG									
A*0301	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*1101	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*1102	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*3001	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*3002	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*3004	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*0201-11	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*0215	-----	-----	-----	-----	-----	-----	*	-----	-----	-----
A*0217	-----	-----	-----	-----	-----	-----	*	-----	-----	-----
A*6801	-----	-----	-----	-----	-----	-----	*	-----	-----	-----
A*6802	-----	-----	-----	-----	-----	A	-----	-----	-----	-----
A*6901	-----	-----	-----	-----	-----	A	-----	-----	-----	-----
A*2301	-----	-----	-----	-----	-----	A	-----	-----	-----	-----
A*2402	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2403	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2404	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2405	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2407	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2501	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*2601	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*3402	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*4301	-----	-----	-----	-----	-----	-----	*	-----	-----	-----
A*6601	-----	-----	-----	-----	-----	-----	*	-----	-----	-----
A*6602	-----	-----	-----	-----	-----	-----	*	-----	-----	-----
A*6603	-----	-----	-----	-----	-----	A	-----	-----	-----	-----
A*2901	-----	-----	-----	-----	-----	A	-----	-----	-----	-----
A*2902	-----	-----	-----	-----	-----	-----	*	-----	-----	-----
A*31012	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*3201	-----	-----	-----	-----	-----	-----	*	-----	-----	-----
A*3301	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*3303	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
A*7401	-----	-----	-----	-----	-----	-----	*	-----	-----	-----
A*7402	-----	-----	-----	-----	-----	-----	*	-----	-----	-----
A*7403	-----	-----	-----	-----	-----	-----	*	-----	-----	-----
A*8001	-----	-----	-----	-----	-----	-----	*	-----	-----	-----

FIG.3D

SUBSTITUTE SHEET (RULE 26)

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HLA-A 5' flankierende Region, Teil V

	410	420	430	440	450
Consensus	TAGGGCATTAGACAGGACTTGACCTGAGGGACTGAGGGTG				
A*0101	-----T-A-----				
A*0301	-----T-A-----				
A*1101	-----T-A-----				
A*1102	-----T-A-----				
A*3001	-----T-A-----				
A*3002	-----T-A-----				
A*3004	-----T-A-----				
A*020111	-----				
A*0215	-----				
A*0217	-----				
A*6801	-----				
A*6802	-----				
A*6901	-----				
A*2301	-----				
A*2402	-----				
A*2403	-----				
A*2404	-----				
A*2405	-----				
A*2407	-----				
A*2501	-----				
A*2601	-----				
A*3402	-----				
A*4301	-----				
A*6601	-----				
A*6602	-----				
A*6603	-----				
A*2901	-----				
A*2902	-----				
A*31012	-----				
A*3201	-----				
A*3301	-----				
A*3303	-----				
A*7401	-----				
A*7402	-----				
A*7403	-----				
A*8001	-----				

FIG.3E

SUBSTITUTE SHEET (RULE 26)

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Consensus	1	10	20	30	40	50	60	70	80	90	100	110	120	130
A*0101	GTGAGTGGGGT	CGGGAGG	GAACGG	CTCT	TGTGGG	GAGCAAG	GGGG	CGCC	CGGAG	AGGG	TCTCGGG	GGGTCT	CAGCCACT	CTCTCGGGCCCGAG
A*0301	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*1101	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*1102	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*3001	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*3002	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*3004	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0201	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0202	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0203	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0204	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0205	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0206	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0207	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0208	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0209	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0210	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0211	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0215	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A*0217	---	---	---	---	---	---	---	---	---	---	---	---	---	---

FIG.4A

SUBSTITUTE SHEET (RULE 26)

10/29

A*6801	C	I	
A*6802	C	I	
A*6901	C	I	
A*2301	C	A	I
A*2402	C	A	I
A*2403	C	A	I
A*2404	C	A	I
A*2405	C	A	I
A*2407	C	A	I
A*2501	C	I	I
A*2601	C	I	I
A*3402	C	I	A
A*6601	C	I	A
A*6602	C	I	A
A*6603	C	I	
A*4301	C	I	
A*2901	C	A	I
A*2902	C	A	I
A*3101	C	I	
A*3201	C	I	
A*3301	C	I	
A*3303	C	I	
A*7401	C	I	
A*7403	C	I	
A*8001	C	I	

FIG.4B

SUBSTITUTE SHEET (RULE 26)

11/29

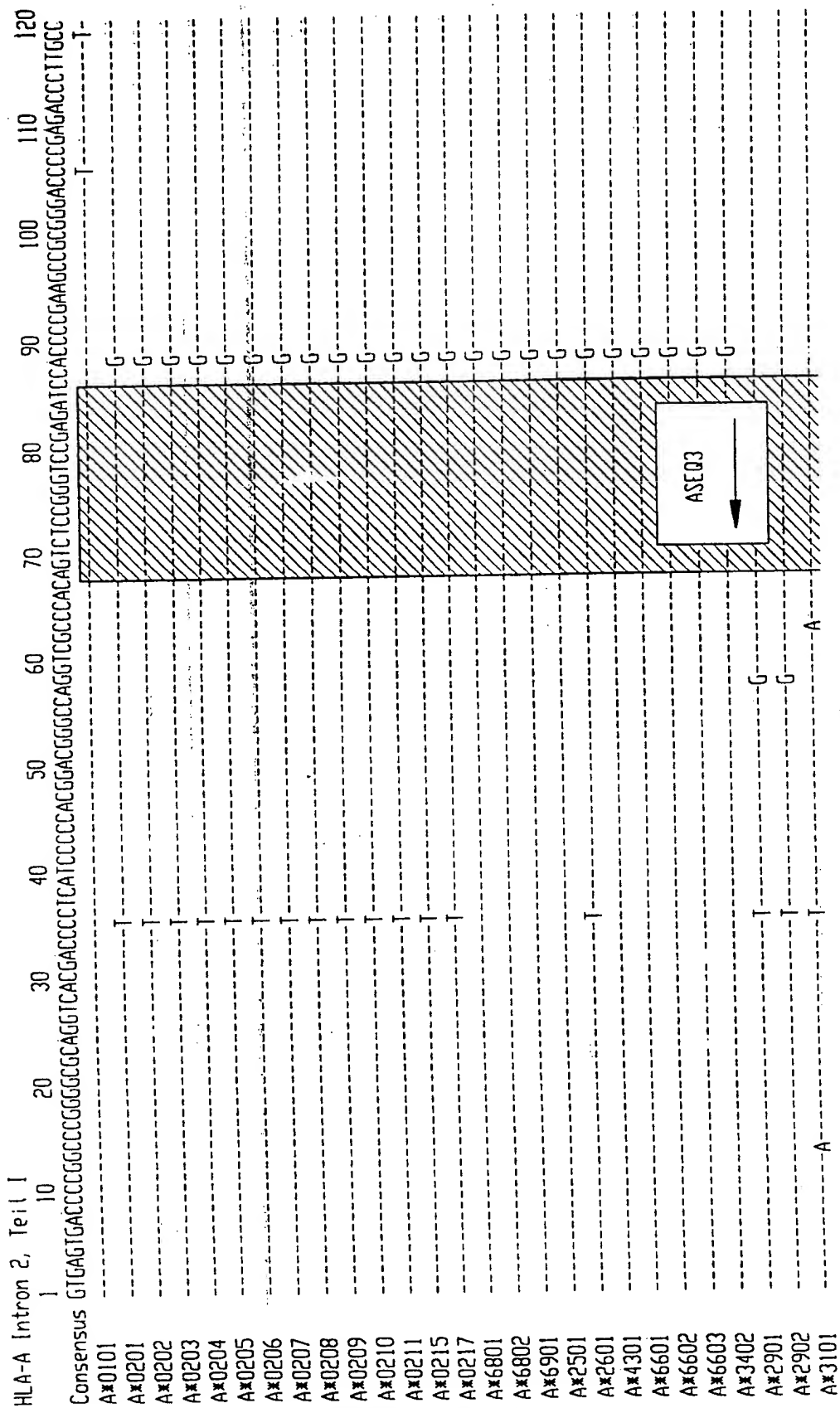


FIG. 5A

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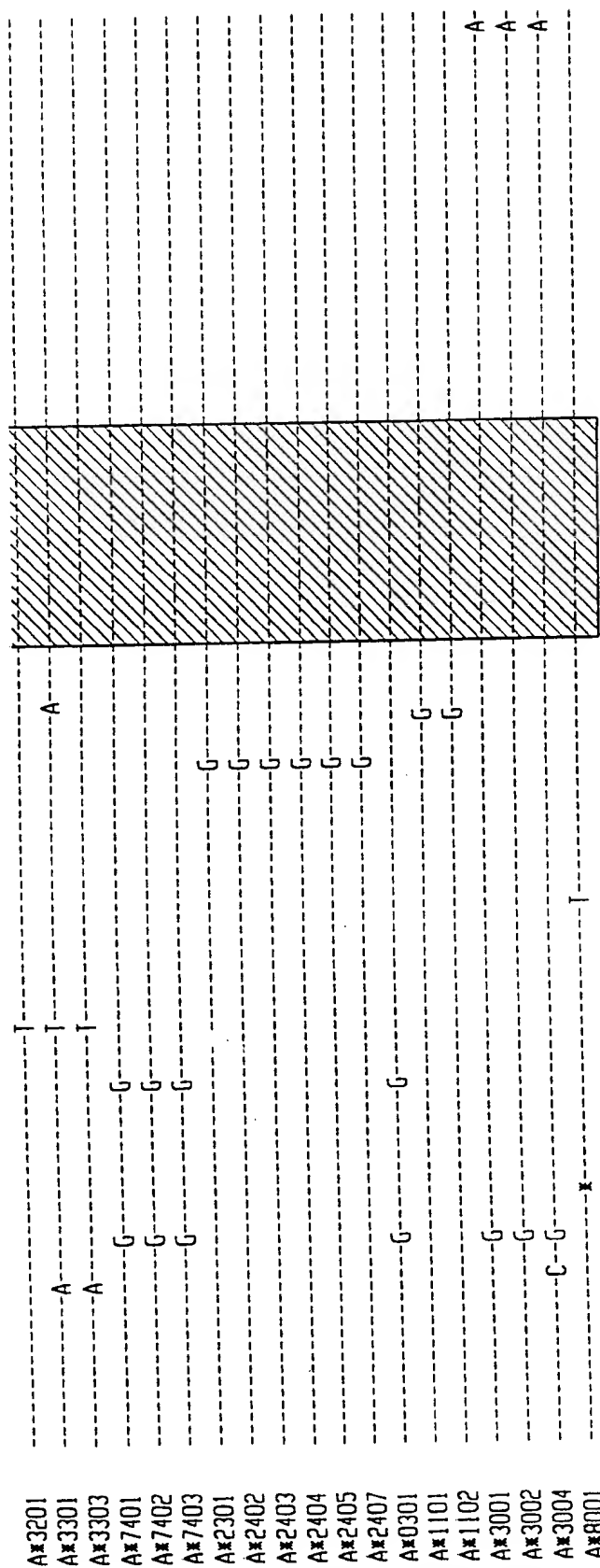


FIG. 5B

SUBSTITUTE SHEET (RULE 26)

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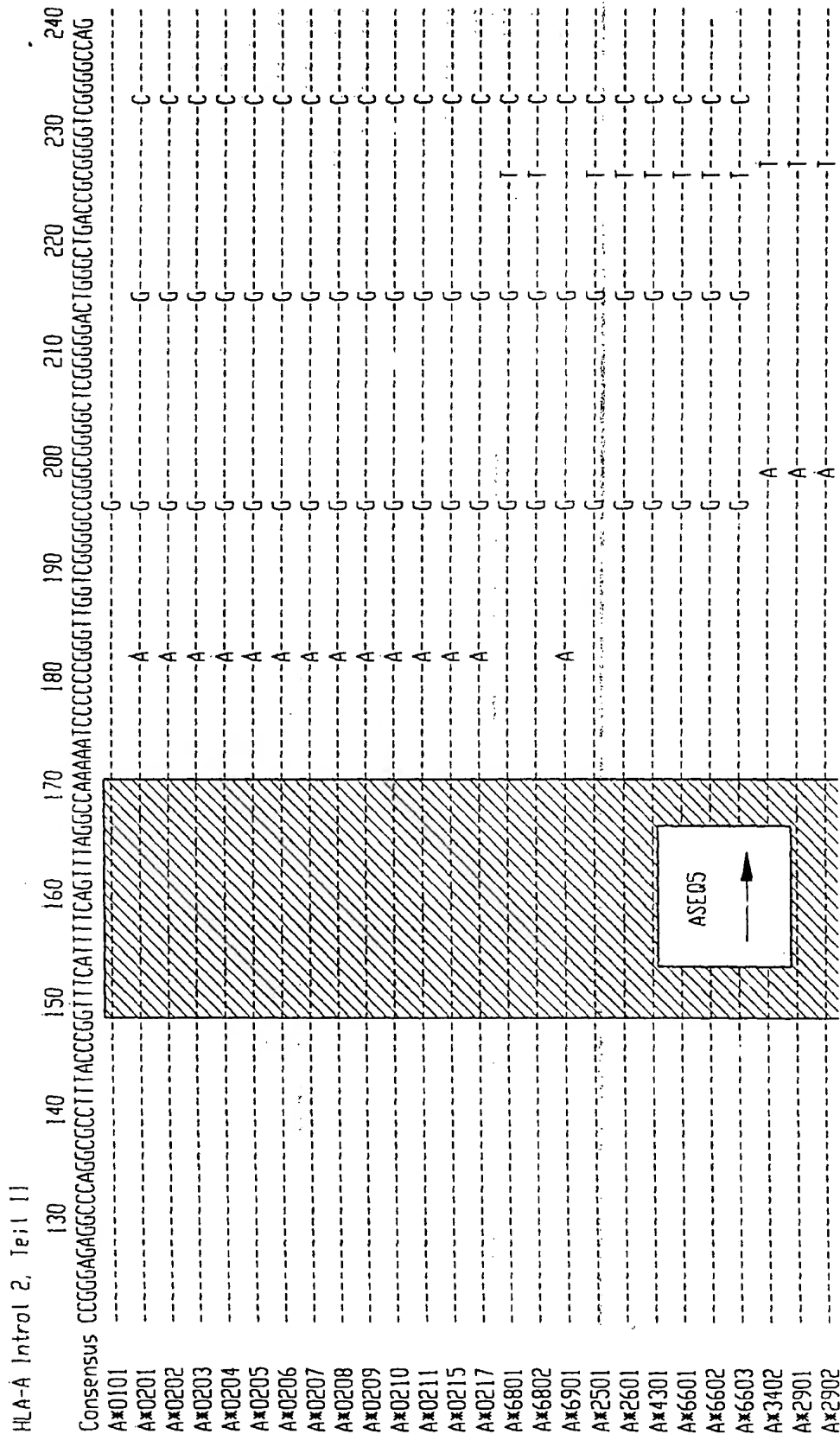


FIG.5C

15/29

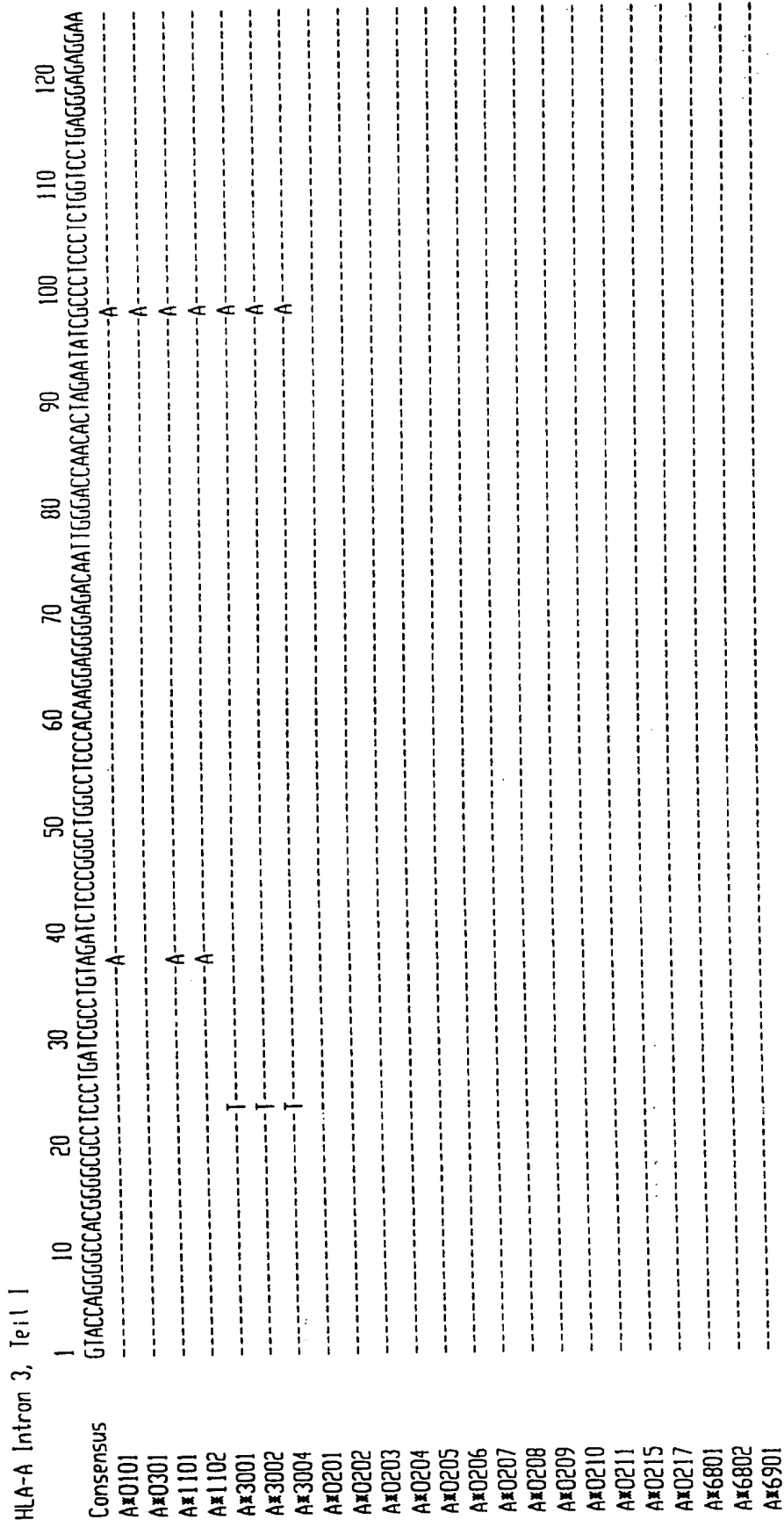


FIG. 6A

SUBSTITUTE SHEET (RULE 26)

16/29

A*2301
A*2402
A*2403
A*2404
A*2405
A*2407
A*2501
A*2601
A*3402
A*4301
A*6601
A*6602
A*6603
A*2901
A*2902
A*3101
A*3201
A*3301
A*3303
A*7401
A*7402
A*7403
A*8001

SUBSTITUTE SHEET (RULE 26)

FIG.6B

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HLA-A Intron 3, Teil II

	130	140	150	160	170	180	190	200	210	220	230	240	250
Consensus	TCCTCTGGGTTTCCAGATCCCTGTACCCAGAGAGTGACTCTGAGGTTCGGCCCTGCTCTGAGCACAAATTAAGGGATAAAAAATCTCTGAGGAATGACCGGGAAGACGATCCCTCGAATACTGATGAGT												
A*0101													
A*0301													
A*1101													
A*1102													
A*3001													
A*3002													
A*3004													
A*0201													
A*0202													
A*0203													
A*0204													
A*0205													
A*0206													
A*0207													
A*0208													
A*0209													
A*0210													
A*0211													
A*0215													
A*0217													
A*6801													
A*6802													

FIG.6C

SUBSTITUTE SHEET (RULE 26)

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A*6901
A*2301
A*2402
A*2403
A*2404
A*2405
A*2407
A*2501
A*2601
A*3402
A*4301
A*6601
A*6602
A*6603
A*2901
A*2902
A*3101
A*3201
A*3301
A*3303
A*7401
A*7402
A*7403
A*8001

SUBSTITUTE SHEET (RULE 26)

FIG.6D

HLA-A Intron 3, Teil III

Consensus

A*0101	XXXX	I
A*0301	XXXX	I
A*1101	XXXX	I
A*1102	XXXX	
A*3001	XXXX	
A*3002	XXXX	
A*3004	XXXX	I
A*0201	A	I
A*0202	A	I
A*0203	A	I
A*0204	A	I
A*0205	A	I
A*0206	A	I
A*0207	A	I
A*0208	A	I
A*0209	A	I
A*0210	A	I
A*0211	A	I
A*0215	A	I
A*0217	A	I
A*6801	A	
A*6802	A	
A*6901	A	I

FIG. 6E

SUBSTITUTE SHEET (RULE 26)

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A*2301	XXXX	A
A*2402	XXXX	A
A*2403	XXXX	A
A*2404	XXXX	A
A*2405	XXXX	A
A*2407	XXXX	A
A*2501		
A*2601		
A*3402		
A*4301		
A*6601		
A*6602		
A*6603		
A*2901		
A*2902		
A*3101		
A*3201		
A*3301		
A*3303		
A*7401		
A*7402		
A*7403		
A*8001		

FIG.6F

SUBSTITUTE SHEET (RULE 26)

HLA-A Intron 3, Teil IV

Consensus	390	400	410	420	430	440	450	460	470	480	490	500
A*0101	ACTCAGGTCAGGACCAGAGTCGCTGCTCCCTGCTTCAGGGACTAGAA	TTTCCACGGGAATAGAGATTATCC	AGGTGCTGCTGGGTTC	GTGCTCCCTTCCCA	TCCCA							
A*0301	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC
A*1101	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC
A*1102	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC
A*3001	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC
A*3002	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC
A*3004	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC	IC
A*0201												
A*0202												
A*0203												
A*0204												
A*0205												
A*0206												
A*0207												
A*0208												
A*0209												
A*0210												
A*0211												
A*0215												
A*0217												
A*6801												

FIG. 6G

A#6802
A#6901
A#2301
A#2402
A#2403
A#2404
A#2405
A#2407
A#2501
A#2601
A#3402
A#4301
A#6601
A#6602
A#6603
A#2901
A#2902
A#3101
A#3201
A#3301
A#3303
A#7401
A#7402
A#7403
A#8001

BNSDOCID: <WO__9826091A2_1_>

FIG. 6H

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HLA-A Intron 3, Teil V

	510	520	530	540	550	560	570	580	590	600
Consensus	GGTGTCCCTGTCATTC	CAAGATAGCCACA	TGCTGGAGGAGTG	TCCCATGACACAGAT	GCAAAATGCC	TGAATGTTCTGACTT	CTCTCTGACAG			
A*0101	---	---	G	---	---	---	---	---	---	C-I
A*0301	---	---	G	---	---	---	---	---	---	C-I
A*1101	---	---	G	---	---	---	---	---	---	C-I
A*1102	---	---	G	---	---	---	---	---	---	C-I
A*3001	---	---	G	---	---	---	---	---	---	C-I
A*3002	---	---	G	---	---	---	---	---	---	C-I
A*3004	---	---	G	---	---	---	---	---	---	C-I
A*0201	---	---	---	---	---	---	---	---	---	A
A*0202	---	---	---	---	---	---	---	---	---	A
A*0203	---	---	---	---	---	---	---	---	---	A
A*0204	---	---	---	---	---	---	---	---	---	A
A*0205	---	---	---	---	---	---	---	---	---	A
A*0206	---	---	---	---	---	---	---	---	---	A
A*0207	---	---	---	---	---	---	---	---	---	A
A*0208	---	---	---	---	---	---	---	---	---	A
A*0209	---	---	---	---	---	---	---	---	---	A
A*0210	---	---	---	---	---	---	---	---	---	A
A*0211	---	---	---	---	---	---	---	---	---	A
A*0215	---	---	---	---	---	---	---	---	---	A
A*0217	---	---	---	---	---	---	---	---	---	A

FIG. 6I

A

A

G CA I C-I
G CA I C-I
G CA I C-I
G CA I C-I
G CA I C-I
G CA I C-I

I
I
I

A G C I C-I
A G C I C-I

SUBSTITUTE SHEET (rule 26)

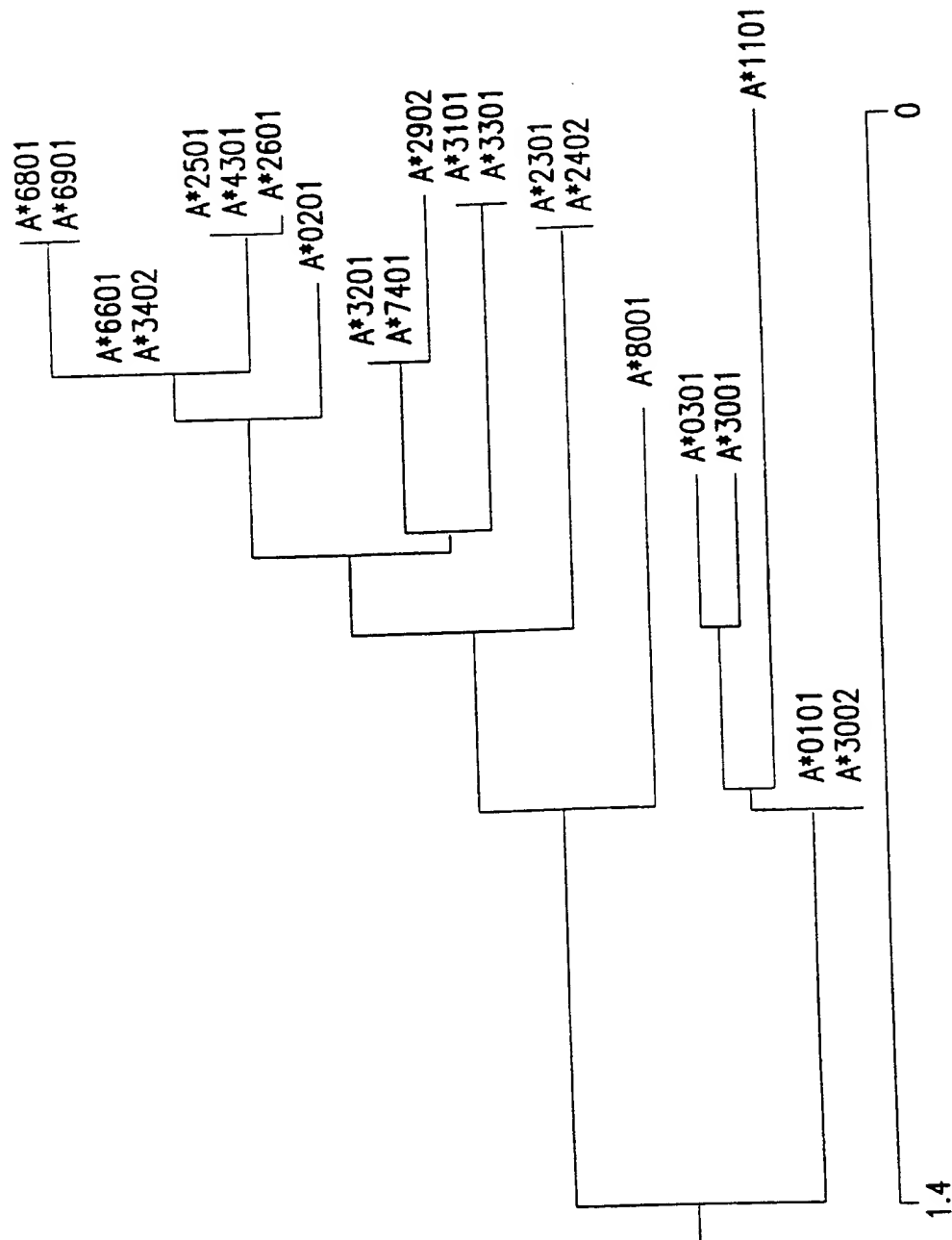


FIG. 7

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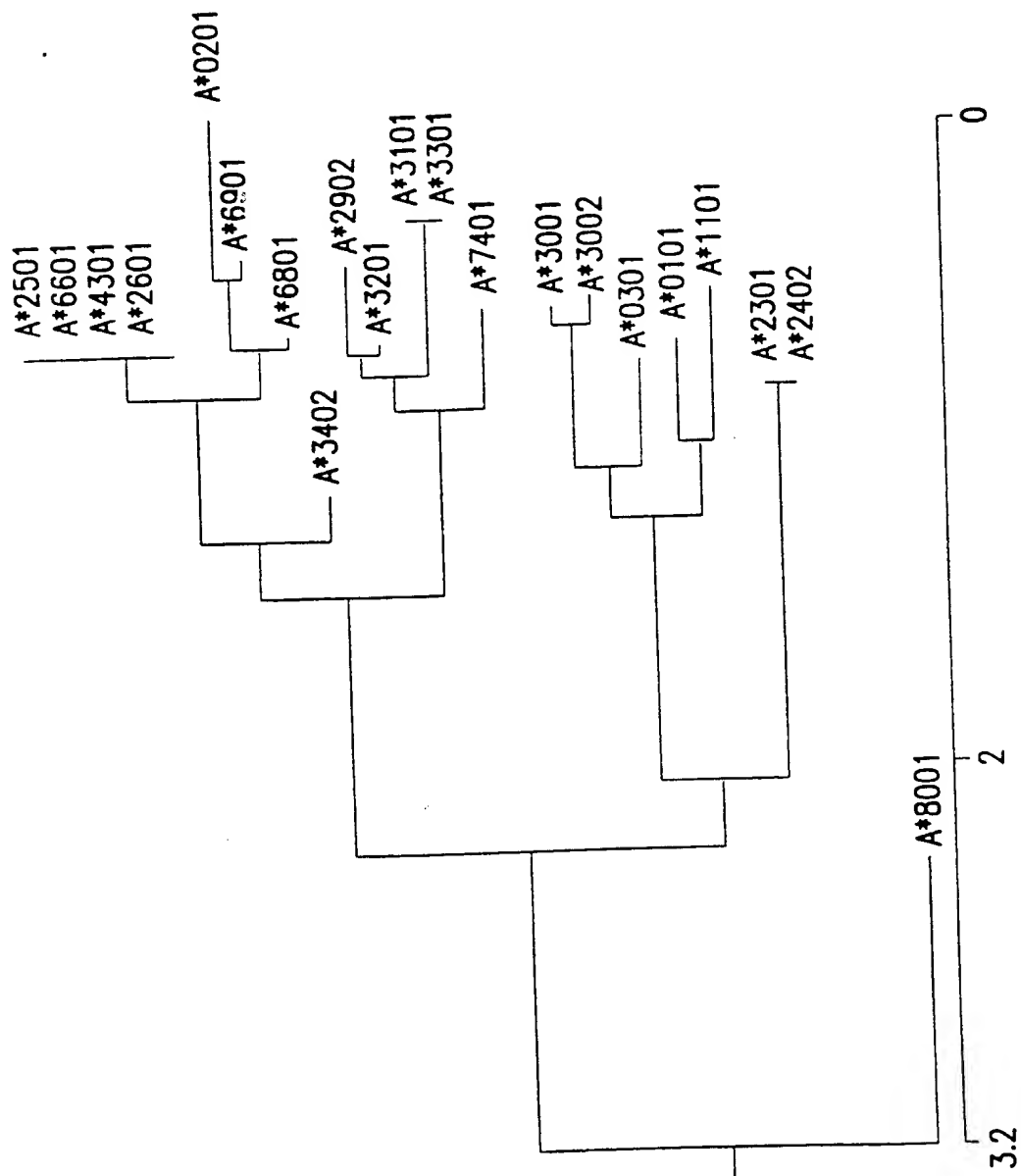
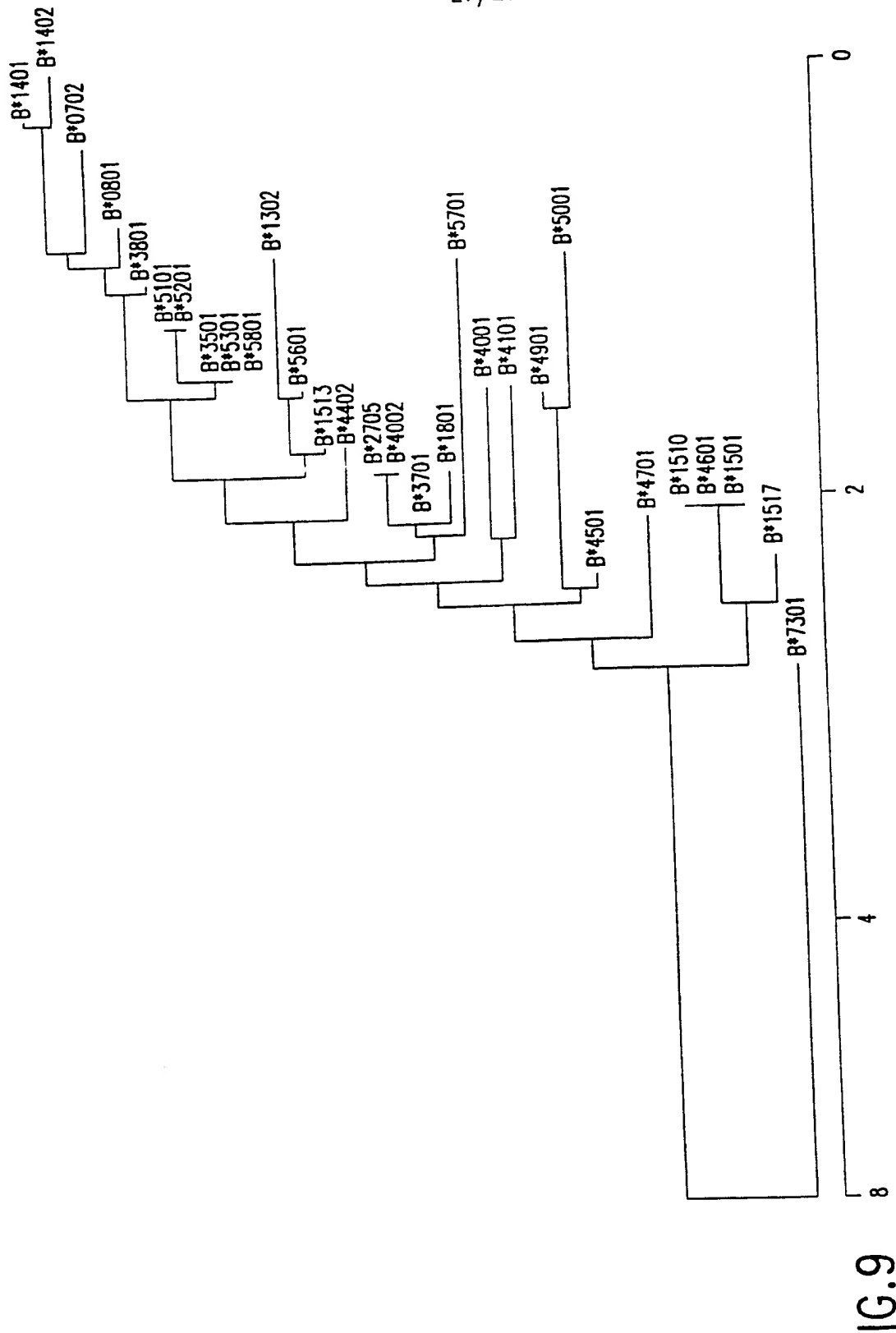


FIG.8

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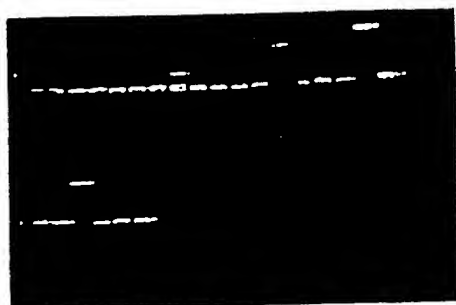


FIG.10

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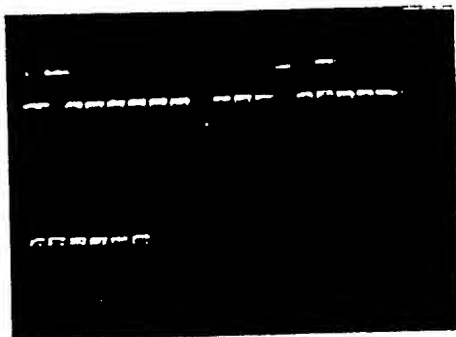


FIG.11

SUBSTITUTE SHEET (rule 26)

1

2

3

4

5

6